

GenCore version 5.1.4_P5-4578
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On protein - protein search, using sw model

Title: US-09-719-748-2
 Perfect score: 1846

Sequence: 1 MEPKQOKVEDFDIGEELG.....TEDDIARRKALHPRRRSSNTS 360

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 Searched: 4569144 seqs, 644733110 residues
 Total number of hits satisfying chosen parameters: 4569144
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Listing First 45 summaries

Database : Pending_Patents_AA_Main,*

1: /cgn2_6/ptodata/1/paa/PCTUS_COMBO.pep:
 2: /cgn2_6/ptodata/1/paa/US06_COMBO.pep:
 3: /cgn2_6/ptodata/1/paa/US07_COMBO.pep:
 4: /cgn2_6/ptodata/1/paa/US08_COMBO.pep:
 5: /cgn2_6/ptodata/1/paa/US081_COMBO.pep:
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 25: /cgn2_6/ptodata/1/paa/US101_COMBO.pep:
 26: /cgn2_6/ptodata/1/paa/US102_COMBO.pep:
 27: /cgn2_6/ptodata/1/paa/US60_COMBO.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	1846	100.0	360	1 PCT-US99-13411-2	Best Local Similarity 100.0%; Pred. No. 4 6e-136; Sequence 1, Appl
2	1846	100.0	360	1 PCT-US99-13411-2	Sequence 2, Appl
3	1846	100.0	360	21 US-09-719-748-2	Sequence 2, Appl
4	1835	99.4	370	21 US-09-731-537-13590	Sequence 13590, A
5	98.8	370	12 US-09-791-537-108109	Sequence 108109, A	
6	1764	95.6	370	21 US-09-791-537-108110	Sequence 108110, A

ALIGNMENTS

RESULT 1
 PCT-US99-13411-2
 ; Sequence 2, Application PC/TUS9913411
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMCHI, Adi
 ; APPLICANT: MCINNIS, A., Patricia
 ; APPLICANT: YEDA RESEARCH AND DEVELOPMENT COMPANY LTD.
 ; TITLE OF INVENTION: DAP-KINASE RELATED PROTEIN
 ; FILE REFERENCE: KIMCHI2A
 ; CURRENT APPLICATION NUMBER: PCT/US99/13411
 ; CURRENT FILING DATE: 1999-06-15
 ; EARLIER APPLICATION NUMBER: 60/089, 294
 ; EARLIER FILING DATE: 1998-06-15
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 360
 ; TYPE: PRT
 ; ORGANISM: Human
 ; PCT-US99-13411-2
 Query Match 100.0%; Score 1846; DB 1; Length 360;
 Best Local Similarity 100.0%; Pred. No. 4 6e-136;
 Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEPKQOKVEDFDIGEELGSGOFAIVKKCRESTGLEYAKFIKKRROSARSGVSEEE 60
 Db 1 MEPKQOKVEDFDIGEELGSGOFAIVKKCRESTGLEYAKFIKKRROSARSGVSEEE 60

Qy 61 IEREVNSILRQVLHNVITLHQYENRTDVHLELVSGGELDFLAQESLSEEEATSF1 120 ; Sequence 108110, Application US/09791537
Db 71 IEREVNSILRQVLHNVITLHQYENRTDVHLELVSGGELDFLAQESLSEEEATSF1 130 ; GENERAL INFORMATION:
; APPLICANT: Biomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791, 537
; CURRENT FILING DATE: 2001-07-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: Patent version 3.0
; SEQ ID NO 108110
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-791-537-108110

RESULT 5
US-09-791-537-108110 ; Sequence 108109, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
; FILE REFERENCE: METHODS OF USE THEREOF
; CURRENT APPLICATION NUMBER: US/09/791, 537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: Patent version 3.0
; SEQ ID NO 108109
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-791-537-108109

Query Match 95.6%; Score 1764; DB: 21; Length: 370;
Best Local Similarity 96.4%; Pred. No. 1; 3e-129; Matches 347; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MEFPKOOKVEDFYDIDGELSGQFATVKCREEKSTGLEYAAFKIKRQSRASRRGYSRE 60 ; Query Match 95.6%; Score 1764; DB: 21; Length: 370;
Db 11 MEFPKOOKVEDFYDIDGELSGQFATVKCREEKSTGLEYAAFKIKRQSRASRRGYSRE 70 ; Best Local Similarity 96.4%; Pred. No. 1; 3e-129; Matches 347; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 61 IEREVNSILRQVLHNVITLHQYENRTDVHLELVSGGELDFLAQESLSEEEATSF1 120 ; Query Match 95.6%; Score 1764; DB: 21; Length: 370;
Db 71 IEREVNSILRQVLHNVITLHQYENRTDVHLELVSGGELDFLAQESLSEEEATSF1 130 ; Best Local Similarity 96.4%; Pred. No. 1; 3e-129; Matches 347; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 181 PEFPKQOKVEDFYDIDGELSGQFATVKCREEKSTGLEYAAFKIKRQSRASRRGYSRE 60 ; Query Match 95.6%; Score 1764; DB: 21; Length: 370;
Db 121 KOILDGVNLYHTKKIAHFDLKPNIMLDKNIPHTKLIDFGLAHEIEDGEVFKNFT 180 ; Best Local Similarity 96.4%; Pred. No. 1; 3e-129; Matches 347; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 61 IEREVNSILRQVLHNVITLHQYENRTDVHLELVSGGELDFLAQESLSEEEATSF1 120 ; Query Match 95.6%; Score 1764; DB: 21; Length: 370;
Db 71 IEREVNSILRQVLHNVITLHQYENRTDVHLELVSGGELDFLAQESLSEEEATSF1 130 ; Best Local Similarity 96.4%; Pred. No. 1; 3e-129; Matches 347; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 121 KOILDGVNLYHTKKIAHFDLKPNIMLDKNIPHTKLIDFGLAHEIEDGEVFKNFT 180 ; Query Match 95.6%; Score 1764; DB: 21; Length: 370;
Db 131 KOILDGVNLYHTKKIAHFDLKPNIMLDKNIPHTKLIDFGLAHEIEDGEVFKNFT 190 ; Best Local Similarity 96.4%; Pred. No. 1; 3e-129; Matches 347; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 181 PEFPKQOKVEDFYDIDGELSGQFATVKCREEKSTGLEYAAFKIKRQSRASRRGYSRE 60 ; Query Match 95.6%; Score 1764; DB: 21; Length: 370;
Db 191 PEFPKQOKVEDFYDIDGELSGQFATVKCREEKSTGLEYAAFKIKRQSRASRRGYSRE 70 ; Best Local Similarity 96.4%; Pred. No. 1; 3e-129; Matches 347; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 241 FSHTSELAKDFIRKLKVETKRKLTDQALRHPWITPVDOQAMVRRESVNLENFRQY 300 ; Query Match 95.6%; Score 1764; DB: 21; Length: 370;
Db 251 FSQTSELAKDFIRKLKVETKRKLTDQALRHPWITPVDOQAMVRRESVNLENFRQY 310 ; Best Local Similarity 96.4%; Pred. No. 1; 3e-129; Matches 347; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 301 VRRWKLSFSIVSLCNHLTRSLMKVHLRDPEDLRNCESDETEEDARRKALHPRRSSTS 360 ; Query Match 95.6%; Score 1764; DB: 21; Length: 370;
Db 311 VRRWKLSFSIVSLCNHLTRSLMKVHLRDPEDLRNCESDETEEDARRKALHPRRSSTS 370 ; Best Local Similarity 96.4%; Pred. No. 1; 3e-129; Matches 347; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

RESULT 7
PCT-US01-08631-39633 ; Sequence 39633, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/5540, 217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649, 167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 39633
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (128)-(147)
; OTHER INFORMATION: TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE domain identified
; OTHER INFORMATION: by eMATRIX, accession number PRO0109B, p-value=7.055e-11, raw
; NAME/KEY: DOMAIN
; RESULT 6
US-09-791-537-108110

LOCATION: (20).-(274) ; OTHER INFORMATION: Eukaryotic protein kinase domain identified by PFam, PCT-US01-08631-39633

Query Match 93.0%; Score 1717; DB 1; Length 359; Best Local Similarity 99.1%; Pred. No. 6.1e-126; Matches 337; Conservative 1; Mismatches 2; Indels 0; Gaps 0; Db 301 STS 360

QY 21 SGQFAIVKKREKGSKYAKTFKRSRQASRRVSVREPIEREVILQVHLHNVITH 80
Db 20 SGQFAIVKKREKGSKYAKTFKRSRQASRRVSVREPIEREVILQVHLHNVITH 79

QY 81 DVEYRDTWVHLEVLGGELDFLAOKESLSEEEATSPFKQIQLDGVNTHTKKLAHFDL 140
Db 80 DVEYRDTWVHLEVLGGELDFLAOKESLSEEEATSPFKQIQLDGVNTHTKKLAHFDL 139

QY 141 KPNIMILDKNIPIPHKLIDFGLAHEIEGVFKNIGPPEFVAPEIVYVPEGLEADM 200
Db 140 KPNIMILDKNIPIPHKLIDFGLAHEIEGVFKNIGPPEFVAPEIVYVPEGLEADM 199

QY 201 WSIGVITYVILLSGASPFLGDTQETLANITSYDDEEFSTSBLAKEFIRKLVKEF 260
Db 200 WSIGVITYVILLSGASPFLGDTQETLANITSYDDEEFSTSBLAKEFIRKLVKEF 259

QY 261 RKRUTQEAIRHPWITPDVNDQAMVRRESVNLNRKQYRRWKLSFSIVSLCNHLTR 320
Db 260 RKRUTQEAIRHPWITPDVNDQAMVRRESVNLNRKQYRRWKLSFSIVSLCNHLTR 319

QY 321 SIMKKVHPRDPDLRNCESTDEEDIARRKALHPRRSSTS 360
Db 320 SLMKVKHLRDPDLRNCESTDEEDIARRKALHPRRSSTS 359

RESULT 8 US-09-791-537-106711

Query Match 70.0%; Score 1293; DB 19; Length 1431; Best Local Similarity 68.2%; Pred. No. 5.9e-52; Matches 242; Conservative 62; Mismatches 43; Indels 8; Gaps 2; Db 1 MTFVRQENBDVYDYGELGSQFATVKKCERKSGLEYAAKFIRKRSRQGVSR 60

QY 1 MTFVRQENBDVYDYGELGSQFATVKKCERKSGLEYAAKFIRKRSRQGVSR 60
Db 1 MTFVRQENBDVYDYGELGSQFATVKKCERKSGLEYAAKFIRKRSRQGVSR 60

QY 61 IEREVSLTQLQVHLHNTLHDVYENRDTWVHLEVLGGELDFLAOKESLSEEEATSPFKQIQLDGVNTHTKKLAHFDL 120
Db 61 IEREVSLTQLQVHLHNTLHDVYENRDTWVHLEVLGGELDFLAOKESLSEEEATSPFKQIQLDGVNTHTKKLAHFDL 120

QY 121 KOILDGVNTHTKKLAHFDLKENTMLDKNIPIPHKLIDFGLAHEIEGVFKNIGT 180
Db 121 KOILDGVNTHTKKLAHFDLKENTMLDKNIPIPHKLIDFGLAHEIEGVFKNIGT 180

QY 181 PEVVAPEIVYVPEGLADEMWSIGVITYILSGASPFLGDTQETLANITSYDDEEF 240
Db 181 PEVVAPEIVYVPEGLADEMWSIGVITYILSGASPFLGDTQETLANITSYDDEEF 240

QY 241 FSHTSELAKDFTRKLKVETRKRTQEAIRHPWITPDVNDQAMVRRESVNLNRKQY 300
Db 241 FSHTSELAKDFTRKLKVETRKRTQEAIRHPWITPDVNDQAMVRRESVNLNRKQY 300

QY 301 VRRWKLSFSIVSLCNHLTRSLMKVH--RDPDLRNCESTDEEDIARRKALH 352
Db 301 ARKKWQSVRLISLCQRLSRSLRSNSMSVARSDTL---DEEDSFVMAIAH 350

RESULT 10 US-09-791-537-49880

Query Match 99.0%; Score 49880; Application US/09791537

General Information: Sequence 49880, Application US/09791537

Applicant: Bionomix, Inc.

Applicant: Debe, Derek

Applicant: Danner, Joseph

Title of Invention: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS

TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 201/210
CURRENT APPLICATION NUMBER: US/09/791, 537
CURRENT FILING DATE: 2001-07-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 49880
LENGTH: 1431
TYPE: PRT
ORGANISM: Homo sapiens
US-09-791-537-49880

Query Match 70.0%; Score 1293; DB 21; Length 1431;
Best Local Similarity 68.2%; Pred. No. 6.9e-92; Matches 242; Conservative 62; Mismatches 43; Indels 8; Gaps 2;

Db 1 MFPFKQOKVVEDYDIDGEBELGSGQFAVKKCRRKSTGLQYAAPIKKRROSRRGSREE 60
Db 61 IEREVSLRQLVHNVTLDHYENRTDVHLELVSGGELDFLAQESSEATF 120
Db 61 IEREVSLKEIQHPNVTLHEVENKTDVILLVELVAGGELDFLAKESTEATF 120

Qy 121 KOILDGVNLHKKIAHFDLKPKENIMLDKNUPIPHKLIDGLAHETEDGEWEFKIFT 180
|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 121 KOILNGVYLYLSQIAHFDLKPKENIMLDKNUPIPHKLIDGLAHETEDGEWEFKIFT 180
Db 121 KOILNGVYLYLSQIAHFDLKPKENIMLDKNUPIPHKLIDGLAHETEDGEWEFKIFT 180

Qy 181 PERVAPETVNPYPLGLEADMWSSIGVITYILSGASPLFGDKTQETLANITSVYDDEF 240
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 181 PERVAPETVNPYPLGLEADMWSSIGVITYILSGASPLFGDKTQETLANITSVYDDEF 240

Qy 241 FSHTSELAKDFTRKLKVETRKRLTOEAIRHPWTPVDNOQAMVRRESVNLLENFKQY 300
|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 241 FSNTSALAKDFTRKLKVDPKKRMTQDSLQHPWKPDQTLQASRSRNSVARSDDTL----DEEDSFVMKAIIH 350
Db 301 ARKKWKSFSIVSLCNHLTRSLMKVHJ--RPDEDFRNCSDETEIDARRKALH 352

RESULT 11
US-60-375-626-6
; Sequence 5, Application US/60375626
; GENERAL INFORMATION:
; APPLICANT: Welch, Nadine
; TITLE OF INVENTION: Methods and compositions for treating
; TITLE OF INVENTION: hematological disorders using 12416, 270, 1410 or 137
; FILE REFERENCE: MP102-065P1(M)
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1431
; TYPE: PRT
; ORGANISM: Homosapien
; US-60-375-626-6

Query Match 70.0%; Score 1293; DB 27; Length 1431;
Best Local Similarity 68.2%; Pred. No. 6.9e-92; Matches 242; Conservative 62; Mismatches 43; Indels 8; Gaps 2;

Db 1 MFPFKQOKVVEDYDIDGEBELGSGQFAVKKCRRKSTGLQYAAPIKKRROSRRGSREE 60
Db 61 IERFQENVDDYDIDGEBELGSGQFAVKKCRRKSTGLQYAAPIKKRROSRRGSREE 60

Qy 61 IERFQENVDDYDIDGEBELGSGQFAVKKCRRKSTGLQYAAPIKKRROSRRGSREE 60
|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 61 IERFQENVDDYDIDGEBELGSGQFAVKKCRRKSTGLQYAAPIKKRROSRRGSREE 60
Db 61 IERFQENVDDYDIDGEBELGSGQFAVKKCRRKSTGLQYAAPIKKRROSRRGSREE 60

Qy 121 KOILDGVNLHKKIAHFDLKPKENIMLDKNUPIPHKLIDGLAHETEDGEWEFKIFT 180
|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 121 KOILDGVNLHKKIAHFDLKPKENIMLDKNUPIPHKLIDGLAHETEDGEWEFKIFT 180
Db 121 KOILDGVNLHKKIAHFDLKPKENIMLDKNUPIPHKLIDGLAHETEDGEWEFKIFT 180

Qy 181 PERVAPETVNPYPLGLEADMWSSIGVITYILSGASPLFGDKTQETLANITSVYDDEF 240
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 181 PERVAPETVNPYPLGLEADMWSSIGVITYILSGASPLFGDKTQETLANITSVYDDEF 240

Qy 241 FSHTSELAKDFTRKLKVETRKRLTOEAIRHPWTPVDNOQAMVRRESVNLLENFKQY 300
|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 241 FSNTSALAKDFTRKLKVDPKKRMTQDSLQHPWKPDQTLQASRSRNSVARSDDTL----DEEDSFVMKAIIH 350
Db 301 ARKKWKSFSIVSLCNHLTRSLMKVHJ--RPDEDFRNCSDETEIDARRKALH 352

RESULT 11
US-08-810-712-10
; Sequence 10, Application US/08810712F
; GENERAL INFORMATION:
; APPLICANT: Yeda Research and Development Co., LTD
; TITLE OF INVENTION: Tumor Suppressor Genes, Proteins Encoded Thereby and
; TITLE OF INVENTION: Use of said Genes and Proteins
; FILE REFERENCE: Yeda-Adi Kimchi
; CURRENT APPLICATION NUMBER: US/08/610, 712F
; CURRENT FILING DATE: 1997-03-03
; EARLIER APPLICATION NUMBER: PCT/US94/11598

EARLIER FILING DATE: 1994-10-12
 NUMBER OF SEQ ID NOS: 31
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 10
 LENGTH: 1423
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-08-810-712-10

Query Match 67.6%; Score 1248; DB 12; Length 1423;
 Best Local Similarity 66.5%; Pred. No. 2.3e-88; Mismatches 43; Indels 16; Gaps 3; Matches 236; Conservative 60; MisMatches 43; Dels 16; Gaps 3;

QY 1 MEPFKQOKVEDFYDGEELSGQFAIVKCRESTGLEYAAFKIKRROSRSRGVSREE 60
 Db 1 MTVFRQENVDYDVGEGELSGQFAVVKCRESTGLEYAFAKEFTRKRTKSSRGVSRED 60

QY 61 IEREVSLILRQHLHNVITLHDVYENRDTWVHILEVSGLGGELDAQKSLSEERATSETI 120
 Db 61 IEREVSLIKEIQHNPVNTLHEVYENKTDTWVHILEVAGELDFLAKESTLEBATEFL 120

QY 121 KQILDGVNLHTKKTAHFDPKPNIMLDKNIPIPHILDFGLAHEIEDGEFKNFT 180
 Db 121 KQILNGVYVYIHLSQLAHFDKPKENIMLDRNPKRKFIDF-----GNEFKNFT 172

QY 181 PEFVAPEIVNYPEPLGLEADMSIGVITYILSGASFLGDTQETIANITSVSDFDEF 240
 Qy 173 PEFVAPEIVNYPEPLGLEADMSIGVITYILSGASFLGDTQETIANITSVSDFDEF 232

QY 241 FSHTSELAKDFTIRKLKVETKRKLTOEARHPWITPVDOQAMRRESVYLNENFRQY 300
 Db 233 FSNTSALAKDFIRRLVLPDKPKRMTOQDSLQHPWKPKDFOALSRSKASAVERMEFKFKA 292

QY 301 VRRWKLSFSIVSLCNHLTRSLMKVHL--RPDEDLNCESSTEEDIARRKALH 352
 Db 293 ARKKWKSVERLISICQRISRSFESRSNNNSVARDDTL---DEEDSFVMKAITH 342

RESULT 14
 US-09-380-159-12
 Sequence 12, Application US/09380159
 GENERAL INFORMATION:
 APPLICANT: Yeda Research and Development Company Ltd.
 TITLE OF INVENTION: Compositions for Treatment Of Disorders Involoving
 FILE REFERENCE: YEDA (KIMCHI)
 CURRENT APPLICATION NUMBER: US/09/380.159
 CURRENT FILING DATE: 1999-08-26
 PRIOR APPLICATION NUMBER: PCT/IL 98/00102
 PRIOR FILING DATE: 1998-03-03
 NUMBER OF SEQ ID NOS: 29
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 12
 LENGTH: 1423
 TYPE: PRT
 ORGANISM: Human
 US-09-380-159-12

Query Match 67.6%; Score 1248; DB 21; Length 1423;
 Best Local Similarity 66.5%; Pred. No. 2.3e-88; Mismatches 43; Indels 16; Gaps 3; Matches 236; Conservative 60; MisMatches 43; Dels 16; Gaps 3;

QY 1 MEPFKQOKVEDFYDGEELSGQFAIVKCRESTGLEYAAFKIKRROSRSRGVSREE 60
 Db 1 MTVFRQENVDYDVGEGELSGQFAVVKCRESTGLEYAFAKEFTRKRTKSSRGVSRED 60

QY 61 IEREVSLILRQHLHNVITLHDVYENRDTWVHILEVSGLGGELDAQKSLSEERATSETI 120
 Db 61 IEREVSLIKEIQHNPVNTLHEVYENKTDTWVHILEVAGELDFLAKESTLEBATEFL 120

QY 121 KQILDGVNLHTKKTAHFDPKPNIMLDKNIPIPHILDFGLAHEIEDGEFKNFT 180
 Db 121 KQILNGVYVYIHLSQLAHFDKPKENIMLDRNPKRKFIDF-----GNEFKNFT 172

QY 181 PEFVAPEIVNYPEPLGLEADMSIGVITYILSGASFLGDTQETIANITSVSDFDEF 240
 Qy 173 PEFVAPEIVNYPEPLGLEADMSIGVITYILSGASFLGDTQETIANITSVSDFDEF 232

QY 241 FSHTSELAKDFTIRKLKVETKRKLTOEARHPWITPVDOQAMRRESVYLNENFRQY 300
 Db 233 FSNTSALAKDFIRRLVLPDKPKRMTOQDSLQHPWKPKDFOALSRSKASAVERMEFKFKA 292

QY 301 VRRWKLSFSIVSLCNHLTRSLMKVHL--RPDEDLNCESSTEEDIARRKALH 352
 Db 293 ARKKWKSVERLISICQRISRSFESRSNNNSVARDDTL---DEEDSFVMKAITH 342

RESULT 15
 US-09-791-537-6033
 Sequence 6033, Application US/09791537
 GENERAL INFORMATION:
 APPLICANT: Bionomix, Inc.
 APPLICANT: Debe, Derek
 APPLICANT: Danter, Joseph
 TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
 TITLE OF INVENTION: METHODS OF USE THEREOF
 FILE REFERENCE: 261/210
 CURRENT APPLICATION NUMBER: US/09/791,537
 CURRENT FILING DATE: 2001-02-22
 NUMBER OF SEQ ID NOS: 153055
 SOFTWARE: Patentin version 3.0
 SEQ ID NO 6033
 LENGTH: 1423
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-791-537-6033

Query Match 67.6%; Score 1248; DB 21; Length 1423;
 Best Local Similarity 66.5%; Pred. No. 2.3e-88; Mismatches 43; Indels 16; Gaps 3; Matches 236; Conservative 60; MisMatches 43; Dels 16; Gaps 3;

QY 1 MEPFKQOKVEDFYDGEELSGQFAIVKCRESTGLEYAAFKIKRROSRSRGVSREE 60
 Db 1 MTVFRQENVDYDVGEGELSGQFAVVKCRESTGLEYAFAKEFTRKRTKSSRGVSRED 60

QY 61 IEREVSLILRQHLHNVITLHDVYENRDTWVHILEVSGLGGELDAQKSLSEERATSETI 120
 Db 61 IEREVSLIKEIQHNPVNTLHEVYENKTDTWVHILEVAGELDFLAKESTLEBATEFL 120

QY 121 KQILDGVNLHTKKTAHFDPKPNIMLDKNIPIPHILDFGLAHEIEDGEFKNFT 180
 Db 121 KQILNGVYVYIHLSQLAHFDKPKENIMLDRNPKRKFIDF-----GNEFKNFT 172

QY 181 PEFVAPEIVNYPEPLGLEADMSIGVITYILSGASFLGDTQETIANITSVSDFDEF 240
 Qy 173 PEFVAPEIVNYPEPLGLEADMSIGVITYILSGASFLGDTQETIANITSVSDFDEF 232

QY 241 FSHTSELAKDFTIRKLKVETKRKLTOEARHPWITPVDOQAMRRESVYLNENFRQY 300
 Db 233 FSNTSALAKDFIRRLVLPDKPKRMTOQDSLQHPWKPKDFOALSRSKASAVERMEFKFKA 292

QY 301 VRRWKLSFSIVSLCNHLTRSLMKVHL--RPDEDLNCESSTEEDIARRKALH 352
 Db 293 ARKKWKSVERLISICQRISRSFESRSNNNSVARDDTL---DEEDSFVMKAITH 342

Search completed: March 26, 2003, 19:16:06
 Job time : 163.064 secs

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Om protein - protein search, using SW model

Run on: March 26, 2003, 19:09:46 ; Search time 28.3146 Seconds
 {without alignments} 1678.167 Million Cell updates/sec

Title: US-09-719-748-2

perfect score: 1846

Sequence: 1 MEPFKQQKVYEDFYDIEELG.....TEEDIARRKALHPRRRSSTS 360

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 613006 seqs, 131990659 residues

Total number of hits satisfying chosen parameters: 613006

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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Pending_Patents_AA_New:*
1: /eogn2_6/pctdata/1/paa/pct_new_comb.pep:*
2: /eogn2_6/pctdata/1/paa/us06_new_comb.pep:*
3: /eogn2_6/pctdata/1/paa/us07_new_comb.pep:*
4: /eogn2_6/pctdata/1/paa/us08_new_comb.pep:*
5: /eogn2_6/pctdata/1/paa/us09_new_comb.pep:*
6: /eogn2_6/pctdata/1/paa/us10_new_comb.pep:*
7: /eogn2_6/pctdata/1/paa/us60_new_comb.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1824	98.8	370	7	US-10-443-566-3011
2	1293	70.0	1431	1	PCT-US03-0248A-38
3	1293	70.0	1431	5	US-09-941-002-377
4	1293	70.0	1431	6	US-10-341-119-220
5	1293	70.0	1436	7	US-60-443-566-4055
6	1224	66.3	1412	5	US-09-941-002-486
7	1166	63.2	454	1	PCT-US02-313-007-119
8	1166	63.2	454	6	US-10-262-445-119
9	1166	63.2	454	7	US-09-445-566-2831
10	1161	62.9	282	5	US-09-724-676-69504
11	1161	62.9	282	5	US-09-724-676-69505
12	1153	62.5	595	5	US-09-724-676-69506
13	1153	62.5	595	6	US-09-724-676-69506
14	677.5	36.7	298	6	US-10-271-978-18
15	668.5	36.2	414	7	US-10-443-566-2540
16	668.5	36.1	2783	6	US-10-365-499-6344
17	664.5	36.0	508	6	US-10-271-978-19
18	641.5	34.8	372	7	US-10-443-566-2980
19	574.5	31.1	596	6	US-10-311-034-6
20	564	30.6	355	6	US-10-250-106-11
21	564	30.6	357	6	US-10-250-106-2
22	564	30.6	357	7	US-10-433-108-2
23	556	30.1	355	6	US-10-355-975-10
24	543.5	29.4	460	7	US-10-443-566-3356
25	543.5	29.4	476	7	US-10-443-566-3355
26	530.5	28.7	370	6	US-10-300-828-4

ALIGNMENTS

RESULT	1
US-60-443-566-3011	
; Sequence 3011, Application US/60443566	
; GENERAL INFORMATION:	
; APPLICANT: CARGILL, Michelle	
; APPLICANT: BEGOVICH, Ann	
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH	
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF	
; FILE REFERENCE: CL00147	
; CURRENT APPLICATION NUMBER: US/60/443,566	
; CURRENT FILING DATE: 2003-01-30	
; NUMBER OF SEQ ID NOS: 25102	
; SOFTWARE: FastSeq for Windows Version 4.0	
; SEQ ID NO: 3011	
; LENGTH: 370	
; TYPE: PRT	
; ORGANISM: Homo sapiens	
; US-60-443-566-3011	

SEQUENCES

Query	Match	Similarity	Score	DB	Length
Best	Local	99.8%	1824	7	370
Matches	357;	Conservative	99.2%	Pred. No.	3e-157;
				Mismatches	2;
				Indels	0;
				Gaps	0;

Sequence 4, Appl

Sequence 18, Appl

Sequence 28, Appl

Sequence 15, Appl

Sequence 88, Appl

Sequence 88, Appl

Sequence 6, Appl

Sequence 176, Appl

Sequence 66, Appl

Sequence 14, Appl

Sequence 687, Appl

Sequence 108, Appl

Sequence 1370, Appl

Sequence 26, Appl

Sequence 19, Appl

Sequence 22, Appl

Sequence 2792, Appl

Sequence 2792, Appl

Sequence 15, Appl

PCT-US03-02484-38
; Sequence 38, Application PC/TUS0302484
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Healy, Aileen
; APPLICANT: Welch, Nadine S.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303, 13906,
; TITLE OF INVENTION: 1513, 17822, 302, 5677, 194, 14393, 28059, 7366, 12212,
; TITLE OF INVENTION: 1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847, 1849,
; FILE REFERENCE: MP10-019
; CURRENT APPLICATION NUMBER: PCT/US03/02484
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/354,333
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: US 60/360,258
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/364,476
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/375,626
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US 60/386,494
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/390,965
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: US 60/392,480
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/394,128
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/399,783
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/403,221
; PRIOR FILING DATE: 2002-08-13
; Remaining prior application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 38
; LENGTH: 1431
; TYPE: PRT
; ORGANISM: Human
; SEQ ID NO: 377
; LENGTH: 1431
; TYPE: PRT
; ORGANISM: Human
; US-09-949-002-377
; Query Match 70.0%; Score 1293; DB 5; Length 1431;
; Best Local Similarity 68.2%; Pred. No. 3e-108;
; Matches 242; Conservative 62; Mismatches 43; Indels 8; Gaps 2;
; QY 1 MEPFKQOKVEDFYDIEGLGSGFAVVKCREEKGSTGLEYAAKFKKRQSRRGSREE 60
; Db 1 MTVFROENVDDYDYGEEGLSGQFAVVKCREEKGSTGLEYAAKFKKRQSRRGSREE 60
; QY 61 TEREVSLROYLHHNVTLDHVYDVEYLHVNTEVYKREKSPGQAKFKKRQSRRGSREE 120
; Db 61 IEREVSLIKEIQHPNVITLHEVYENKTDVILVLEVAGGLEDFLAKESEBATEFL 120
; Qy 121 KOILDGVNLYLTKKKAHFDPKPNIMLDKINPIPHIKLDFGLAHETEONGVERNIGT 180
; Db 121 KQILNQVYVYLHSQIAHFDKPNIMLDKINPIPHIKLDFGLAHETEONGVERNIGT 180
; Qy 181 PEFAVAPENYEPGLEADMWISGTYLISGASPLGSTQKETLANTSVSDFDEEF 240
; Db 181 PEFAVAPENYEPGLEADMWISGTYLISGASPLGSTQKETLANTSVSDFDEEF 240
; Qy 241 FSHTSELAKDIRKLWKEPDKRJLQIAHLRHPMTPWDQAMRRESTYLNENFKOY 300
; Db 241 FSNTSALAKDFTRRLVLPDKPKRMTOQSLQHPWPKDQALSRKASAQNMEFKFKA 300
; Qy 301 VRRWKLSFSVLCHLRLSMKVKHL-RPDEUDRNCSDTEDIANRKHAL 352
; Db 301 ARKKWKSQRTLSLCRLRSPLSNSNMVARSDPDL---DEDSFVMAITH 350
; RESULT 3
; US-09-949-002-377
; Sequence 377, Application US/09949002
; GENERAL INFORMATION:
; APPLICANT: Venet, J Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CL00793
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 1083
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 377
; LENGTH: 1431
; TYPE: PRT
; ORGANISM: Human
; US-09-949-002-377
; Query Match 70.0%; Score 1293; DB 6; Length 1431;
; Best Local Similarity 68.2%; Pred. No. 3e-108;
; Matches 242; Conservative 62; Mismatches 43; Indels 8; Gaps 2;
; QY 1 MEPEKKQOKVEDFYDIEGLGSGFAVVKCREEKGSTGLEYAAKFKKRQSRRGSREE 60
; Db 1 MTVPFQENVDDYDYGEEGLSGQFAVVKCREEKGSTGLEYAAKFKKRQSRRGSREE 60
; QY 61 TEREVSLROYLHHNVTLDHVYDVEYLHVNTEVYKREKSPGQAKFKKRQSRRGSREE 120
; Db 61 IEREVSLIKEIQHPNVITLHEVYENKTDVILVLEVAGGLEDFLAKESEBATEFL 120
; Qy 121 KOILDGVNLYLTKKKAHFDPKPNIMLDKINPIPHIKLDFGLAHETEONGVERNIGT 180
; Db 121 KQILNQVYVYLHSQIAHFDKPNIMLDKINPIPHIKLDFGLAHETEONGVERNIGT 180
; Qy 181 PEFAVAPENYEPGLEADMWISGTYLISGASPLGSTQKETLANTSVSDFDEEF 240
; Db 181 PEFAVAPENYEPGLEADMWISGTYLISGASPLGSTQKETLANTSVSDFDEEF 240
; Qy 241 FSHTSELAKDIRKLWKEPDKRJLQIAHLRHPMTPWDQAMRRESTYLNENFKOY 300
; Db 241 FSNTSALAKDFTRRLVLPDKPKRMTOQSLQHPWPKDQALSRKASAQNMEFKFKA 300
; RESULT 4
; US-10-348-119-220
; Sequence 220, Application US/10348119
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTI
; TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KIN
; TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
; FILE REFERENCE: D0185 NP
; CURRENT APPLICATION NUMBER: US/10/348,119
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: US 60/350,061
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 795
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 220
; LENGTH: 1431
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-348-119-220
; Query Match 70.0%; Score 1293; DB 6; Length 1431;

Best Local Similarity 68.2%; Pred. No. 3e-108; Indels 8; Gaps 2; Matches 242; Conservative 62; Mismatches 43;

Query 1 MPPFKQOKVEDDYDIEGELGSGFAIYKCCRSTGLEAAFKIKRROSRRRGVSREE 60
 DB 1 MPPFKQOKVEDDYDIEGELGSGFAIYKCCRSTGLEAAFKIKRROSRRRGVSREE 60
 Query 61 IEREVSLRQVIAHNVTLHDVYENRTDVHTELGSGFQAVVKCRRKSTGQAKFIRRTRSSRGVSRED 60
 DB 61 IEREVSLRQVIAHNVTLHDVYENRTDVHTELGSGFQAVVKCRRKSTGQAKFIRRTRSSRGVSRED 60
 Query 121 KQILDGYNYLHKKKTAIFDKRENTMUDKNPIPHKLINGBLAIEDEWEKFNGT 180
 DB 121 KQILDGYNYLHKKKTAIFDKRENTMUDKNPIPHKLINGBLAIEDEWEKFNGT 180
 Query 181 PFPVAPETVNEVPLGLADEMWASIGVITYILSGASPLGDTKQETANITSYDDEF 240
 DB 181 PFPVAPETVNEVPLGLADEMWASIGVITYILSGASPLGDTKQETANITSYDDEF 240
 Query 301 VERRWKLSFSTISLCNLTSRKVHL--RPDEDLRNCSDEEDDIARRKALH 352
 DB 301 VERRWKLSFSTISLCNLTSRKVHL--RPDEDLRNCSDEEDDIARRKALH 352
 Result 5 US-60-443-566-4055
 Sequence 4055, Application US/60443566
 General Information:
 Applicant: CARGILL, Michele
 Title of Invention: GENETIC POLYMORPHISMS ASSOCIATED WITH FILE REFERENCE: C1001447
 Current Application Number: US/60/443, 566
 Current Filing Date: 2003-01-30
 Number of Seq ID Nos: 25102
 Software: FastSEQ for Windows Version 4.0
 Seq ID No: 4055
 Length: 1436
 Type: PRT
 Organism: Homo sapiens
 US-60-443-566-4055

Query Match 66.3%; Score 1224; DB 5; Length 1412;
 Best Local Similarity 68.5%; Pred. No. 5.4e-102; Mismatches 58; Matches 231; Conservative 58; Gaps 8; Gaps 2; Indels 8;

Query 19 LGSGQFAIYKCCRSTGLEAAFKIKRROSRRRGVSREE 78
 DB 1 LFGSQFAVVKKREKSTGQAKFIRRTRSSRGVSRED 60
 Query 79 LHVVENRTDVHTELGSGFQAVVKCRRKSTGQAKFIRRTRSSRGVSRED 138
 DB 61 LHEVYENRTDVHTELGSGFQAVVKCRRKSTGQAKFIRRTRSSRGVSRED 120
 Query 139 DLKPENIMLDKNPIPHKLIDFGLAIEDEGEVFKNFGTPFPVAPETVNEVPLGLA 198
 DB 121 DLKPENIMLDKNPIPHKLIDFGLAIEDEGEVFKNFGTPFPVAPETVNEVPLGLA 180
 Query 199 DMNSIGVITYILSGASPLGDTKQETANITSYDDEFSEHTSBLAKDFIRKLVK 258
 DB 181 DMNSIGVITYILSGASPLGDTKQETANITSYDDEFSEHTSBLAKDFIRKLVK 240
 Query 259 ETRKRLTQEARHPWTPVDNOQAMRRESVNLFRQVRRMKLSPISIVSLCNHL 318
 DB 241 DPKKRMTQDSLQHPWPKPDKDQALSRSKASAVNMMEKFKA 300

Query Match 70.0%; Score 1293; DB 7; Length 1436;
 Best Local Similarity 68.2%; Pred. No. 3e-108; Mismatches 43; Indels 8; Gaps 2; Matches 242; Conservative 62; Gaps 2; Indels 8; Mismatches 43;

Query 1 MPPFKQOKVEDDYDIEGELGSGFAIYKCCRSTGLEAAFKIKRROSRRRGVSREE 60
 DB 1 MPPFKQOKVEDDYDIEGELGSGFAIYKCCRSTGLEAAFKIKRROSRRRGVSREE 60
 Result 7 PCR-US02-31357-119
 Sequence 119, Application PC/US0231357
 General Information:
 Applicant: Curagen Corporation, et al.
 Title of Invention: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHOD
 File Reference: 21402-465D-061
 Current Application Number: PCR/US02/31357
 Current Filing Date: 2002-10-02
 Prior Application Number: 60/327,454
 Prior Filing Date: 2001-10-05
 Prior Application Number: 60/327,917
 Prior Filing Date: 2001-10-09
 Prior Application Number: 60/328,029
 Prior Filing Date: 2001-10-09
 Prior Application Number: 60/328,056
 Prior Filing Date: 2001-10-09
 Prior Application Number: 60/328,849
 Prior Filing Date: 2001-10-12

Query 241 FSHTSELAKDFTRKLYKETRKRLLTQEARHPWTPVDNOQAMRRESVNLFRQV 300
 DB 241 FSHTSELAKDFTRKLYKETRKRLLTQEARHPWTPVDNOQAMRRESVNLFRQV 300
 Query 301 VRRWKLSFSTISLCNLTSRKVHL--RPDEDLRNCSDEEDDIARRKALH 352

PRIOR APPLICATION NUMBER: 60/329,414 ;
 PRIOR FILING DATE: 2001-10-15 ;
 PRIOR APPLICATION NUMBER: 60/330,142 ;
 PRIOR FILING DATE: 2001-10-17 ;
 PRIOR APPLICATION NUMBER: 60/341,058 ;
 PRIOR FILING DATE: 2001-10-22 ;
 PRIOR APPLICATION NUMBER: 60/343,629 ;
 PRIOR FILING DATE: 2001-10-24 ;
 PRIOR APPLICATION NUMBER: 60/349,575 ;
 PRIOR FILING DATE: 2001-10-29 ;
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 133 ;
 SOFTWARE: CuraseqList version 0.1 ;
 SEQ ID NO: 119 ;
 LENGTH: 454 ;
 TYPE: PRT ;
 ORGANISM: Homo sapiens ;
 PCT US02 31357-119 ;

 Query Match 63.2%; Score 1166; DB 1; Length 454;
 Best Local Similarity 64.7%; Pred. No. 1. 9e-97; Mismatches 49; Indels 18; Gaps 3; Matches 233; Conservative 49; ;

 Qy 1 MEPKOQKQVDFYDGFEGELSGQFAIVKKGREKFTGLEYAAKFKKRQKRASRQGVSRRE 60 ;
 Db 1 MSTFROEDVEDHYEMGEELSGQFAIVKKGROKGITKEYAAKFKKRQKRASRQGVSRRE 60 ;

 Qy 61 IEREVSLRQLHVNVITLHDVYENTDVHILEVSGLPFLDFIAOKSSLSEERATFSI 120 ;
 Db 61 IEREVNLRLRHPNITLHDIFENKTDVHILEVSGGLDFIAEKSSLTEDEATQFL 120 ;

 Qy 121 KQILDGVNYLHTKTAHFDKPENIMLDKNIPHIKLIDFGLAHEIEDGVKNIFT 180 ;
 Db 121 KQILDGVHYLHSKTAHFDPKPNIMLDKNIPNPKLIDFGTAHKAGNERKNIFT 180 ;

 Qy 181 PEFAPEIVNVEPLGLEADMSIGVITYILISGASPFLGDTQKELANTISVSVDDEF 240 ;
 Db 181 PEFAPEIVNVEPLGLEADMSIGVITYILISGASPFLGDTQKELANTISVSVDDEF 240 ;

 Qy 241 FSHTSLSLAKDFTIRKLKVKEETKRLTQEARLHPWTPVDDQAMYRRESVNLNRKQY 300 ;
 Db 241 FSNTSELAKDFTIRKLKVKEETKRLTQEARLHPWTPVDDQAMYRRESVNLNRKQY 300 ;

 Qy 301 VRRWKLSFSTVSLCNHLTRSLMKVHLRPE--DLRNCSDETDIARRKALHPRRS 357 ;
 Db 294 RRRKTRKLTKEYTIKS-----LPPNNSYADFERSKVLEAAAEGRELORS 345 ;

 RESULT 8
 US-0-262-445-119
 Sequence 119, Application US/10262445 ;
 GENERAL INFORMATION:
 ; APPLICANT: Alsobrook II, John
 ; APPLICANT: Burgess, Catherine
 ; APPLICANT: Catterton, Elina
 ; APPLICANT: Chant, John
 ; APPLICANT: Chaudhuri, Amitabha
 ; APPLICANT: Edinger, Shlomit
 ; APPLICANT: Glotz, Loic
 ; APPLICANT: Gorman, Linda
 ; APPLICANT: Guo, Xiaojia
 ; APPLICANT: Kekuda, Ramesh
 ; APPLICANT: Mezes, Peter
 ; APPLICANT: Millet, Isabelle
 ; APPLICANT: Ooi, Chean Eng
 ; APPLICANT: Patterson, Meera
 ; APPLICANT: Reiger, Daniel
 ; APPLICANT: Saptok, Kimberly
 ; APPLICANT: Taupier Jr., Raymond J.
 ; APPLICANT: Zerhusen, Bryan
 ; APPLICANT: Zhong, Haibong
 ; APPLICANT: Zhong, Mel ;

 RESULT 9
 US-0-443-566-2831
 Sequence 2831, Application US/60443566 ;
 GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; APPLICANT: BEGOVICH, Ann
 ; APPLICANT: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL00147
 ; CURRENT APPLICATION NUMBER: US/60/443,566

Query Match 62.5%; Score 1153; DB 5; Length 595;
 Best Local Similarity 78.5%; Pred. No. 4.2e-96;
 Matches 216; Conservative 38; Mismatches 21; Indels 0; Gaps 0;

QY 1 MEPPKQKVEDFYDIDGEEGLSGQFAIVKCREKSTGLEYAAFKIKKRQSARSGRSVREE 60
 1 MSTFRQEDVEDHBMGEELSGQFAIVKCRQKGKEYAAFKIKKRQSARSGRSVREE 60
 Db 1 MSTFRQEDVEDHBMGEELSGQFAIVKCRQKGKEYAAFKIKKRQSARSGRSVREE 60

QY 61 IERVSILRQVLHNVTLDVYENRTDVHILEVLSGGELDFLAQESLSBEATSF1 120
 1 IERVSILRQVLHNVTLDVYENRTDVHILEVLSGGELDFLAQESLSBEATSF1 120
 Db 61 IEREVNLIRERHNNTIDHIFENKTIDWVLLILEVLSGGELDFLAQESLSBEATSF1 120

QY 121 KQIDGVHVLHSKRLAHFDLKPENIMLUDKNVNPRKLIDFGIAHKTEAGNEFKNFGT 180
 121 KQIDGVHVLHSKRLAHFDLKPENIMLUDKNVNPRKLIDFGIAHKTEAGNEFKNFGT 180

Db 181 PERVAPETVNYEPLIGELEADMWSIGVITYILSGASPFGETKQBTLNISAVNDFDEY 240
 181 PERVAPETVNYEPLIGELEADMWSIGVITYILSGASPFGETKQBTLNISAVNDFDEY 240

QY 241 FSHSELAKOFIRKLUVKTRKTRKTOEALRHPI 275
 241 FSHSELAKOFIRKLUVKTRKTRKTOEALRHPI 275

Db 241 FSNTSELAKDFIRKLUVKPDKRMTAQSLHSWI 275
 241 FSNTSELAKDFIRKLUVKPDKRMTAQSLHSWI 275

RESULT 13
 US-09-724-676A-69506

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEAR
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; FILE REFERENCE: CLO00921-CIP-DIV
 ; CURRENT APPLICATION NUMBER: US/10/274,978
 ; CURRENT FILING DATE: 2002-10-22
 ; PRIORITY NUMBER: 09/858,664
 ; PRIORITY NUMBER: 09/858,664
 ; PRIORITY NUMBER: 09/711,134
 ; PRIORITY NUMBER: 09/711,134
 ; PRIORITY NUMBER: 2001-05-17
 ; PRIORITY NUMBER: 2001-05-17
 ; PRIORITY NUMBER: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 34
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 18
 ; LENGTH: 298
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-10-274-978-18

Query Match 36.7%; Score 677.5; DB 6; Length 298;
 Best Local Similarity 45.0%; Pred. No. 2e-53; Mismatches 136; Conservative 56; Indels 15; Gaps 5;

Db 55 IMNCUHLPKVLCVOCDAFEERKANVMLEIVSGBELFERTIDDEFELTERECTIKYMRQISE 114
 QY 7 OKVDFYDIDGEEGLSGQFAIVKCREKSTGLEYAAFKIKKRQSARSGRSVREE 66
 7 OKVDFYDIDGEEGLSGQFAIVKCREKSTGLEYAAFKIKKRQSARSGRSVREE 66

Db 126 GVYHTKKAFAHFDLKPENIMLUDKNVNPRKLIDFGIAHKTEAGNEFKNFGTPEVA 185
 126 GVYHTKKAFAHFDLKPENIMLUDKNVNPRKLIDFGIAHKTEAGNEFKNFGTPEVA 185

Db 115 GVEVTHKQCVIHLDPKEMIMCVMK-T-GTRKLUIDGLARRIENAGSLVKVLFGTPEVA 172
 115 GVEVTHKQCVIHLDPKEMIMCVMK-T-GTRKLUIDGLARRIENAGSLVKVLFGTPEVA 172

QY 186 PEVINYEPLIGELEADMWSIGVITYILSGASPFGETKQBTLNITSVSYDDEFSHTS 245
 186 PEVINYEPLIGELEADMWSIGVITYILSGASPFGETKQBTLNITSVSYDDEFSHTS 245

Db 173 PEVINYEPLISYATDMSIGVITYILSGASPFGETKQBTLNITSVSYDDEFSHTS 232
 173 PEVINYEPLISYATDMSIGVITYILSGASPFGETKQBTLNITSVSYDDEFSHTS 232

Db 246 ELAKOFIRKLUVKTRKTRKTOEALRHPI-TPVNDQQAMVRBRSVNLNFRIQYRR 304
 246 ELAKOFIRKLUVKTRKTRKTOEALRHPI-TPVNDQQAMVRBRSVNLNFRIQYRR 304

Db 233 DDAKDFISNLKDMNRDCTOCLQHPMLMDTKNMEA---KKLSKDRMKYMAR 287
 233 DDAKDFISNLKDMNRDCTOCLQHPMLMDTKNMEA---KKLSKDRMKYMAR 287

QY 305 WK 306
 305 WK 306

Db 288 WQ 289
 288 WQ 289

RESULT 14
 US-10-274-978-18

; Sequence 13; Application US/10/274,978
 ; GENERAL INFORMATION:
 ; APPLICANT: WEI, Ming-Hui, et al

Query Match 62.5%; Score 1153; DB 5; Length 595;
 Best Local Similarity 78.5%; Pred. No. 4.2e-96;
 Matches 216; Conservative 38; Mismatches 21; Indels 0; Gaps 0;

QY 1 MEFPKQOKVEDFYDIDGELGSQFAIVKCREKSTGLEYAAFKIKKRQSARSGRSVREE 60
 1 MSTFRQEDVEDHBMGEELSGQFAIVKCRQKGKEYAAFKIKKRQSARSGRSVREE 60
 Db 1 MSTFRQEDVEDHBMGEELSGQFAIVKCRQKGKEYAAFKIKKRQSARSGRSVREE 60

QY 61 IEREVSLRQVLHNVTLDVYENRTDVHILEVLSGGELDFLAQESTSEATSF1 120
 61 IEREVSLRQVLHNVTLDVYENRTDVHILEVLSGGELDFLAQESTSEATSF1 120

Db 61 IEREVNLIRERHNNTIDHIFENKTIDWVLLILEVLSGGELDFLAQESTSEATSF1 120

QY 121 KQIDGVHVLHSKRLAHFDLKPENIMLUDKNVNPRKLIDFGIAHKTEAGNEFKNFGT 180
 121 KQIDGVHVLHSKRLAHFDLKPENIMLUDKNVNPRKLIDFGIAHKTEAGNEFKNFGT 180

Db 181 PERVAPETVNYEPLIGELEADMWSIGVITYILSGASPFGETKQBTLNISAVNDFDEY 240
 181 PERVAPETVNYEPLIGELEADMWSIGVITYILSGASPFGETKQBTLNISAVNDFDEY 240

QY 241 FSNTSELAKDFIRKLUVKPDKRMTAQSLHSWI 275
 241 FSNTSELAKDFIRKLUVKPDKRMTAQSLHSWI 275

Db 241 FSNTSELAKDFIRKLUVKPDKRMTAQSLHSWI 275
 241 FSNTSELAKDFIRKLUVKPDKRMTAQSLHSWI 275

RESULT 14
 US-10-274-978-18

; Sequence 13; Application US/10/274,978
 ; GENERAL INFORMATION:
 ; APPLICANT: WEI, Ming-Hui, et al

Query Match 36.2%; Score 668.5; DB 7; Length 414;
 Best Local Similarity 38.9%; Pred. No. 2.1e-52; Mismatches 139; Conservative 78; Mismatches 95; Indels 45; Gaps 9;

QY 2 EPFKQOKVEDFYDIDGELGSQFAIVKCREKSTGLEYAAFKIKKRQSARSGRSV-R 58
 2 EPFKQOKVEDFYDIDGELGSQFAIVKCREKSTGLEYAAFKIKKRQSARSGRSV-R 58

Db 53 EPF---DGYSLCPGRELRGKEAVYRKQIKSOGKEAKFMRK---RKQDCR 102
 53 EPF---DGYSLCPGRELRGKEAVYRKQIKSOGKEAKFMRK---RKQDCR 102

OY	EEIRENSILROVLHIN--VTLHDYVNTDUDVHLLELVS GGELED--FLAQKESLSEE 114
Db	MEIHEIAVL ELAQDPWNVNHLHEYETASEMILVLEYAAGGETFDQCVADREERFEK 161
103	:: :: :: :: : : : :
OY	115 EATSFROIOLGDGVNLYHTKAFKAHDPKENPMLDKNIPIHKLIFGLAHETIEGVEF 174
Db	DVQRLMRQIOLLEGVHFUHLTRDVHLDKQPONILTSSES -PLGDIKUVDFGLRSILRKELLE 220
162	:: :: :: :: : : : :
OY	175 KNIFCTPEFAPEVNPYEPGLSEADWMISGVITYLLSGASPFGLDTKOELANITSVY 234
Db	: :: :: :: :: : : : :
221	REIMGTPEVAPAEIISYDPMATDMWSIGVLYTVMGTSPFLGNDKOETFLNTSQWL 280
OY	235 DFEDEFHSWSELAKEFIRKLKVKEFRKRLTQEARHPWTPVDQNOAMWRESVNL 294
Db	:: :: :: :: : : : :
281	SYEREFEDVLAESAVFIRTLVKKPBDRATAECKPWHQPTQSSTOEPSFRMKEALEA 340
OY	295 NFRKQVRRWRKLSFSVTSLCNHLTRSLMMKKVHLRDEDLRNCSDEOTDEETARRKL 351
341	N----- ALQEGHSVPEINSIDKSKTEESTIVEELI 371
Db	

Search completed: March 26, 2003, 19:17:03
Job time : 31.3146 secs

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On protein - protein search, using sw model

Run on: March 26, 2003, 19:04:06 ; search time 116.936 seconds
 (without alignments) (without alignments)
 1450.068 Million cell updates/sec

Title: US-09-719-748-2_COPY_13_275

Perfect score: 1343

Sequence: 1 YDGFEEELSGQFAVKKCRE.....LVKETRKRLTICEARLRHPWI 263

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%, Listing First 45 summaries

Database : Pending_Patents_AA_Main,*

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2: /cgn2_6/ptodata/1/paa/us06_comb.pep:*

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25: /cgn2_6/ptodata/1/paa/us102_comb.pep:*

26: /cgn2_6/ptodata/1/paa/us60_comb.pep:*

27: /cgn2_6/ptodata/1/paa/us60_comb.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1

PCT-US99-13411-2

; Sequence 2, Application PCT/TUS9913411

; GENERAL INFORMATION:

; APPLICANT: KIMCHI, Adi

; APPLICANT: MCINTYRE, Patricia

; APPLICANT: YEDA RESEARCH AND DEVELOPMENT COMPANY LTD.

; TITLE OF INVENTION: DAP KINASE RELATED PROTEIN

; FILE REFERENCE: KIMCHI2A

; CURRENT APPLICATION NUMBER: PCT/US99/13411

; CURRENT FILING DATE: 1999-06-15

; EARLIER APPLICATION NUMBER: 60/089,294

; EARLIER FILING DATE: 1998-06-15

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO: 2

; LENGTH: 360

; TYPE: PRT

; ORGANISM: Human

PCT-US99-13411-2

Query Match 100.0% ; Score 1343; DB 1; Length 360;

Best Local Similarity 100.0%; Pred. No. 1 1e-102;

Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YDGFEEELSGQFAVKKCRE.....LVKETRKRLTICEARLRHPWI 60

Dy 13 YDGFEEELSGQFAVKKCRE.....LVKETRKRLTICEARLRHPWI 72

PRIORITY FILING DATE: 1998-06-15
 NUMBER OF SEQ ID NOS: 14
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 2
 LENGTH: 360
 TYPE: PRT
 ORGANISM: Human
 ; US-09-719-748-2

RESULT 2
 PCT-US99-13411-2
 ; Sequence 2, Application PC/TUS9913411A
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMCHI, Adi
 ; APPLICANT: MCINNIS A., Patricia
 ; APPLICANT: YEDA RESEARCH AND DEVELOPMENT COMPANY LTD.
 ; TITLE OF INVENTION: DAP-KINASE RELATED PROTEIN
 ; FILE REFERENCE: KIMCHI2A
 ; CURRENT APPLICATION NUMBER: PCT/US99/13411A
 ; CURRENT FILING DATE: 1999-06-15
 ; EARLIER APPLICATION NUMBER: 60/089,294
 ; EARLIER FILING DATE: 1998-06-15
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 2
 ; LENGTH: 360
 ; TYPE: PRT
 ; ORGANISM: Human

PC-T-US99-13411-2

Query Match 100.0%; Score 1343; DB 1; length 360;
 Best Local Similarity 100.0%; Pred. No. 1.1e-102; Indels 0; Gaps 0;
 Matches 263; Conservative 0; Mismatches 0;

1 YDGEELSGQFATVKKCREKSTGLEYAAFKIKRQSRSRVSRETEREVSILRQL 60
 13 YDGEELSGQFATVKKCREKSTGLEYAAFKIKRQSRSRVSRETEREVSILRQL 72
 133 KKIAHFDLKPEPINMLDKNIPIPHKLIDGLAHEIEDGVEFKNIFGTPFPEVAPIVNE 192

QY 1 YDGEELSGQFATVKKCREKSTGLEYAAFKIKRQSRSRVSRETEREVSILRQL 60
 QY 13 YDGEELSGQFATVKKCREKSTGLEYAAFKIKRQSRSRVSRETEREVSILRQL 72
 QY 61 HHNVTILHDYENRTDVHILEVLNSGELDFLAQESLSEEBATSIKOILDGVNLHT 120
 Db 73 HHNVTILHDYENRTDVHILEVLNSGELDFLAQESLSEEBATSIKOILDGVNLHT 132

QY 121 KKIAHFDLKPEPINMLDKNIPIPHKLIDGLAHEIEDGVEFKNIFGTPFPEVAPIVNE 180
 Db 133 KKIAHFDLKPEPINMLDKNIPIPHKLIDGLAHEIEDGVEFKNIFGTPFPEVAPIVNE 192

QY 181 PLGLEADMWSIGVITYILSGASPLGDTQETLANITSVSYDFDEEFSSHTSBLAKDFI 240
 Db 193 PLGLEADMWSIGVITYILSGASPLGDTQETLANITSVSYDFDEEFSSHTSBLAKDFI 252

QY 241 RKLVVIETRKRLTQEARLHPWI 263
 Db 253 RKLVVIETRKRLTQEARLHPWI 275

RESULT 3
 US-09-719-748-2
 ; Sequence 2, Application US/09719748
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMCHI, Adi
 ; TITLE OF INVENTION: DAP-KINASE RELATED PROTEIN
 ; FILE REFERENCE: KIMCHI2A
 ; CURRENT APPLICATION NUMBER: US/09/719,748
 ; CURRENT FILING DATE: 2000-12-15
 ; PRIORITY APPLICATION NUMBER: 60/089,294

RESULT 4
 US-09-791-537-13590
 ; Sequence 13590, Application US/09791537
 ; GENERAL INFORMATION:
 ; APPLICANT: Bionomix, Inc.
 ; APPLICANT: Danzer, Derek
 ; APPLICANT: Denzer, Joseph
 ; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY
 ; TITLE OF INVENTION: METHODS OF USE THEREOF
 ; FILE REFERENCE: 261/210
 ; CURRENT APPLICATION NUMBER: US/09/791,537
 ; CURRENT FILING DATE: 2001-02-22
 ; NUMBER OF SEQ ID NOS: 153055
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 13590
 ; LENGTH: 370
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-791-537-13590

Query Match 99.2%; Score 1332; DB 21; Length 370;
 Best Local Similarity 99.6%; Pred. No. 9.3e-102; Indels 1; Gaps 0;
 Matches 262; Conservative 0; Mismatches 1;

1 YDGEELSGQFATVKKCREKSTGLEYAAFKIKRQSRSRVSRETEREVSILRQL 60
 13 YDGEELSGQFATVKKCREKSTGLEYAAFKIKRQSRSRVSRETEREVSILRQL 82
 121 KKIAHFDLKPEPINMLDKNIPIPHKLIDGLAHEIEDGVEFKNIFGTPFPEVAPIVNE 180
 Db 83 HHNVTILHDYENRTDVHILEVLNSGELDFLAQESLSEEBATSIKOILDGVNLHT 142

QY 61 HHNVTILHDYENRTDVHILEVLNSGELDFLAQESLSEEBATSIKOILDGVNLHT 120
 Db 143 KKIAHFDLKPEPINMLDKNIPIPHKLIDGLAHEIEDGVEFKNIFGTPFPEVAPIVNE 180
 QY 181 PLGLEADMWSIGVITYILSGASPLGDTQETLANITSVSYDFDEEFSSHTSBLAKDFI 240
 Db 203 PLGLEADMWSIGVITYILSGASPLGDTQETLANITSVSYDFDEEFSSHTSBLAKDFI 262

Query Match 83.7%; Score 1124; DB 1; Length 263;
 Best Local Similarity 79.5%; Pred. No. 1.e-84; 13; Indels 0; Gaps 0;
 Matches 209; Conservative 41; Mismatches 13; Gaps 0;

RESULT 8
 PCT-US99-13411-3
 ; Sequence 3, Application PC/TUS9913411
 ; GENERAL INFORMATION:
 ; APPLICANT: MCINNIS A., Patricia
 ; APPLICANT: YEDA RESEARCH AND DEVELOPMENT COMPANY LTD.
 ; TITLE OF INVENTION: DAP-KINASE RELATED PROTEIN
 ; CURRENT APPLICATION NUMBER: PCT/US99/13411
 ; CURRENT FILING DATE: 1999-06-15
 ; EARLIER APPLICATION NUMBER: 60/089, 294
 ; EARLIER FILING DATE: 1998-06-15
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 263
 ; TYPE: PRT
 ; ORGANISM: Human
 ; PCT-US99-13411-3

Query Match 83.7%; Score 1124; DB 1; Length 263;
 Best Local Similarity 79.5%; Pred. No. 1.e-84; 13; Indels 0; Gaps 0;
 Matches 209; Conservative 41; Mismatches 13; Gaps 0;

QY 1 YDGEELSGSGOFATYKCREKSTGLEYAAKFIIKKRQSRRGSREETEREVSIROLVL 60
 Db 1 YDGEELSGSGOFAVVKCREEKGTYAAKFIIKKRQSRRGSRETEREVSIROLVL 60

QY 61 HNVVITLHVENVNTDYLVELVSGELDFLAKESESSEATSIKQILDGVNLHT 120
 Db 61 HPNVVITLHEVENKTDVILVELVAGELDFLAKESESSEATSIKQILDGVNLHT 120

QY 121 KTAHFDLKPEIMLDKNIPHIKLIDGFLAHELEDGYEFKNFGTPPERVAPIVNE 180
 Db 121 LQAHFDLKPEIMLDNRVPKRKTDIFGLAKHIDFGNEFKNFGTPPERVAPIVNE 180

QY 181 PGLEADMWNSIGVITYILSASPLFGDTKETELANITSYSDDEFESTSELAKDFI 240
 Db 181 PGLEADMWNSIGVITYILSASPLFGDTKETELANVSAVNEYEEDEYFSNTSALAKDFI 240

QY 241 RKLVKETRKRKTRTQEARLHPWI 263
 Db 241 RRLVVDPKRMQTQDSLQHPWI 263

RESULT 10
 US-09-719-748-3
 ; Sequence 3, Application US/09/19748
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMCHI, Adi
 ; TITLE OF INVENTION: DAP-KINASE RELATED PROTEIN
 ; TITLE REFERENCE: KIMCHI2A
 ; CURRENT APPLICATION NUMBER: US/09/19748
 ; CURRENT FILING DATE: 2000-12-15
 ; PRIOR APPLICATION NUMBER: 60/089, 294
 ; PRIOR FILING DATE: 1998-06-15
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 263
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-09-719-748-3

Query Match 83.7%; Score 1124; DB 21; Length 263;
 Best Local Similarity 79.5%; Pred. No. 1.e-84; 13; Indels 0; Gaps 0;
 Matches 209; Conservative 41; Mismatches 13; Gaps 0;

QY 1 YDGEELSGSGOFATYKCREKSTGLEYAAKFIIKKRQSRRGSRETEREVSIROLVL 60
 Db 1 YDGEELSGSGOFAVVKCREEKGTYAAKFIIKKRQSRRGSRETEREVSIROLVL 60

QY 61 HNVVITLHVENVNTDYLVELVSGELDFLAKESESSEATSIKQILDGVNLHT 120
 Db 61 HPNVVITLHEVENKTDVILVELVAGELDFLAKESESSEATSIKQILDGVNLHT 120

QY 121 KTAHFDLKPEIMLDKNIPHIKLIDGFLAHELEDGYEFKNFGTPPERVAPIVNE 180
 Db 121 LQAHFDLKPEIMLDNRVPKRKTDIFGLAKHIDFGNEFKNFGTPPERVAPIVNE 180

QY 181 PGLEADMWNSIGVITYILSASPLFGDTKETELANITSYSDDEFESTSELAKDFI 240
 Db 181 PGLEADMWNSIGVITYILSASPLFGDTKETELANVSAVNEYEEDEYFSNTSALAKDFI 240

QY 241 RKLVKETRKRKTRTQEARLHPWI 263
 Db 241 RRLVVDPKRMQTQDSLQHPWI 263

RESULT 9
 PCT-US99-13411-3
 ; Sequence 3, Application PC/TUS9913411A
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMCHI, Adi
 ; APPLICANT: MCINNIS A., Patricia
 ; APPLICANT: YEDA RESEARCH AND DEVELOPMENT COMPANY LTD.
 ; TITLE OF INVENTION: DAP-KINASE RELATED PROTEIN
 ; TITLE REFERENCE: KIMCHI2A
 ; CURRENT APPLICATION NUMBER: PCT/US99/13411A
 ; CURRENT FILING DATE: 1999-06-15
 ; EARLIER APPLICATION NUMBER: 60/089, 294
 ; EARLIER FILING DATE: 1998-06-15
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 263
 ; TYPE: PRT
 ; ORGANISM: Human
 ; PCT-US99-13411-3

Query Match 83.7%; Score 1124; DB 1; Length 263;
 Best Local Similarity 79.5%; Pred. No. 1.e-84; 13; Indels 0; Gaps 0;
 Matches 209; Conservative 41; Mismatches 13; Gaps 0;

QY 121 KTAHFDLKPEIMLDKNIPHIKLIDGFLAHELEDGYEFKNFGTPPERVAPIVNE 180
 Db 121 LQAHFDLKPEIMLDNRVPKRKTDIFGLAKHIDFGNEFKNFGTPPERVAPIVNE 180

QY 181 PGLEADMWNSIGVITYILSASPLFGDTKETELANITSYSDDEFESTSELAKDFI 240
 Db 181 PGLEADMWNSIGVITYILSASPLFGDTKETELANVSAVNEYEEDEYFSNTSALAKDFI 240

QY 241 RKLVKETRKRKTRTQEARLHPWI 263
 Db 241 RRLVVDPKRMQTQDSLQHPWI 263

RESULT 11
 US-09-538-092-1198
 ; Sequence 1198, Application US/09538092
 ; GENERAL INFORMATION:

APPLICANT: Giot, Loic
 TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
 FILE REFERENCE: 15966-542
 CURRENT APPLICATION NUMBER: US/09/538,092
 PRIORITY FILING DATE: 2000-03-29
 PRIORITY APPLICATION NUMBER: 60/127,352
 PRIORITY FILING DATE: 1999-04-01
 NUMBER OF SEQ ID NOS: 1387
 SOFTWARE: CuratSeqFormatter version 0.9
 SEQ ID NO: 1198
 LENGTH: 1431
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (0)..(0)
 OTHER INFORMATION: Polypeptide Accession Number B53355
 US-09-538,092-1198
 Query Match 83.7%; Score 1124; DB 19; Length 1431;
 Best Local Similarity 79.5%; Pred. No. 9.8e-84; Matches 209; Conservative 41; Mismatches 13; Indels 0; Gaps 0;
 Qy 1 YDIGEBELGSQFATVKCREEKSTGLEAAFKIKRROSRRGVSREEREVSIQLRQL 60
 Db 13 YDTGEELGSQFAVVKCREEKSTGLEAAFKIKRROSRRGVSREEREVSIKEIQ 72
 Qy 61 HNNVITLHDYENRTDVHILEVLSGGELDFLAQESLSEEAATSIKIQILDGVNLYLT 120
 Db 73 HPNVITLHEVNEYKTIDVILILEVAGGEFLAKESLSEEAETEFLQILGVYLYHS 132
 Qy 121 KKIAHFDLKPEINIMLDKNIPIPHKLIDGLAREIDEDWEEKFNGTPFPEVAIVNYE 180
 Db 133 LQIAHFDLKPEINIMLDKNIPIPHKLIDGLAREIDEDWEEKFNGTPFPEVAIVNYE 192
 Qy 181 PLGLEADMWSIGVITYILSGASPLGDKOETLANITSYDDEFSHTSELAKDFI 240
 Db 193 PLGLEADMWSIGVITYILSGASPLGDKOETLANVSAVNEYEFEDYSNTSALAKDFI 252
 Qy 241 RKLVYKTRKRLTQEARLHPWI 263
 Db 253 RRLVYKDPKKRMQTODSLQHPWI 275
 RESULT 12
 US-09-791-537-49880
 Sequence 49880, Application US/09791537
 GENERAL INFORMATION:
 APPLICANT: Bionomix, Inc.
 APPLICANT: Debe, Derek
 APPLICANT: Danzer, Joseph
 TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
 TITLE OF INVENTION: METHODS OF USE THEREOF
 FILE REFERENCE: 261/210
 CURRENT APPLICATION NUMBER: US/09/791,537
 CURRENT FILING DATE: 2001-02-22
 NUMBER OF SEQ ID NOS: 153055
 SOFTWARE: Patentin version 3.0
 SEQ ID NO: 49880
 LENGTH: 1431
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-791-537-49880
 Query Match 83.7%; Score 1124; DB 21; Length 1431;
 Best Local Similarity 79.5%; Pred. No. 9.8e-84; Matches 209; Conservative 41; Mismatches 13; Indels 0; Gaps 0;
 Qy 1 YDIGEBELGSQFATVKCREEKSTGLEAAFKIKRROSRRGVSREEREVSIQLRQL 60
 Db 13 YDTGEELGSQFAVVKCREEKSTGLEAAFKIKRROSRRGVSREEREVSIKEIQ 72
 Qy 61 HNNVITLHDYENRTDVHILEVLSGGELDFLAQESLSEEAATSIKIQILDGVNLYLT 120
 Db 73 HPNVITLHEVNEYKTIDVILILEVAGGEFLAKESLSEEAETEFLQILGVYLYHS 132
 Qy 121 KKIAHFDLKPEINIMLDKNIPIPHKLIDGLAREIDEDWEEKFNGTPFPEVAIVNYE 180
 Db 133 LQIAHFDLKPEINIMLDKNIPIPHKLIDGLAREIDEDWEEKFNGTPFPEVAIVNYE 192
 Qy 181 PLGLEADMWSIGVITYILSGASPLGDKOETLANITSYDDEFSHTSELAKDFI 240
 Db 193 PLGLEADMWSIGVITYILSGASPLGDKOETLANVSAVNEYEFEDYSNTSALAKDFI 252
 Qy 241 RKLVYKTRKRLTQEARLHPWI 263
 Db 253 RRLVYKDPKKRMQTODSLQHPWI 275
 RESULT 14
 US-60-375,626-6
 Sequence 6, Application US/60375626
 GENERAL INFORMATION:
 APPLICANT: Weich, Nadine
 TITLE OF INVENTION: Methods and compositions for treating
 TITLE OF INVENTION: hematological disorders using 12416, 270, 1410 or 137
 FILE REFERENCE: MP102-063P(M)
 CURRENT APPLICATION NUMBER: US/60/375,626
 CURRENT FILING DATE: 2002-04-26
 NUMBER OF SEQ ID NOS: 8

SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 6
 LENGTH: 1431
 TYPE: PRT
 ORGANISM: Homosapien
 US-60-375-626-6

Query Match 83.7%; Score 1124; DB 27; Length 1431;
 Best Local Similarity 79.5%; Pred. No. 9 8e-84;
 Matches 209; Conservative 41; Mismatches 13; Indels 0; Gaps 0;

OY 1 YDGEELGSGQFAIVKKCREKSTGLEVAFKIKRQSRAASRRGSVRSREIEREVSILOVL 60
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 ||| YDTGEELGSGQFAVKKCREKSTGLOYAAKFKIKRQSRAASRRGSVRSREIEREVSILOVL 72
 Db 13 HINVTILHDVVENRNDVHIELVSGEELDFELAQKESLSSEAFATSIKQILDGVNLYLT 120
 |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 QY 61 HINVTILHDVVENRNDVHIELVSGEELDFELAQKESLSSEAFATSIKQILDGVNLYLT 72
 ||| LQIAHFDLKPENIMLDRNVRPKRIIDFGLAHKDIFGNEPKNIFGTPEFVAPETVNE 192
 Db 73 HPNVITLHEVENKTVDVILLLELVAGGELDFPLAERESTEEATEFLKIQLINGVYLLHS 132
 QY 121 KRIAHPDLKPENIMLDRNVRPKRIIDFGLAHKDIFGNEPKNIFGTPEFVAPETVNE 180
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 133 LQIAHFDLKPENIMLDRNVRPKRIIDFGLAHKDIFGNEPKNIFGTPEFVAPETVNE 192
 QY 181 PLGLEDAMWMSIGVITYLISGRASPFEGDTKQETPLANTISVSIDFDEFEFFSHSELAKDFI 240
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 193 PLGLEDAMWMSIGVITYLISGRASPFEGDTKQETPLANTISVSIDFDEFEFFSHSELAKDFI 252
 QY 241 RKLKVKETRKRLTIQEALRHFWI 263
 |||:|||||:|||||:
 Db 253 RRLVVKDPKRMTOQDSLQHPWI 275
 QY 254 RRLVVKDPKRMTOQDSLQHPWI 275

RESULT 15
 US-09-719-748-4
 ; Sequence 4, Application US/09/19748
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMCHI, Ad1
 ; TITLE OF INVENTION: DAP-KINASE RELATED PROTEIN
 ; FILE REFERENCE: KIMCHI2A
 ; CURRENT APPLICATION NUMBER: US/09/719, 748
 ; CURRENT FILING DATE: 2000-12-15
 ; PRIOR APPLICATION NUMBER: 60/089,294
 ; PRIOR FILING DATE: 1998-06-15
 ; NUMBER OF SEQ ID NOS: 14
 ; SEQ ID NO 4
 ; LENGTH: 263
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-09-719-748-4

Query Match 83.5%; Score 1121; DB 21; Length 263;
 Best Local Similarity 79.8%; Pred. No. 1 9e-84;
 Matches 210; Conservative 36; Mismatches 17; Indels 0; Gaps 0;

OY 1 YDGEELGSGQFAIVKKCREKSTGLEVAFKIKRQSRAASRRGSVRSREIEREVSILOVL 60
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 1 YENGELGSGQFAIVRKCRQKGICKEYAKFKIKRQLSSRRGSVRSREIEREVNLRLR 60
 QY 61 HNWVITLHDVVENRNDVHIELVSGEELDFELAQKESLSSEAFATSIKQILDGVNLYLT 120
 |||:|||||:|||||:|||||:|||||:|||||:
 Db 61 HPNVITLHDIFENKTDVVLLLELVSGEELDFPLAERESTEEATEFLKQILDGVNLYLT 120
 QY 121 KKAHFDLKPENIMLDRNVRPKRIIDFGLAHKDIFGNEPKNIFGTPEFVAPETVNE 180
 |||:|||||:|||||:|||||:
 Db 121 KKAHFDLKPENIMLDRNVRPKRIIDFGLAHKDIFGNEPKNIFGTPEFVAPETVNE 180
 QY 181 PLGLEDAMWMSIGVITYLISGRASPFEGDTKQETPLANTISVSIDFDEFEFFSHSELAKDFI 240
 |||:|||||:
 Db 181 PLGLEDAMWMSIGVITYLISGRASPFEGDTKQETPLANTISVSIDFDEFEFFSHSELAKDFI 240
 QY 241 RKLKVKETRKRLTQEALRHFWI 263
 |||:|||||:
 Db 241 RRLVVKDPKRMTOQDSLQHPWI 275

Search completed: March 26, 2003, 19:16:09
 Job time : 119.936 secs

Gencore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 19:09:46 ; Search time 20.6854 Seconds

Sequence: (without alignments) 1678.167 Million cell updates/sec

Title: US-09-719-748-2_COPY_13_275

Perfect score: 1343

Sequence: 1 YDGEELGSGQFAIVKKCRE.....LVKHTRKRLTIQEALRHPWI 263

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 613006 seqs, 131990659 residues

Total number of hits satisfying chosen parameters: 613006

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Pending_Patents_AA_New;*

1: /cgn2_6/pdataa/1/paa/us06_new_comb.pep:*

2: /cgn2_6/pdataa/1/paa/us07_new_comb.pep:*

3: /cgn2_6/pdataa/1/paa/us08_new_comb.pep:*

4: /cgn2_6/pdataa/1/paa/us09_new_comb.pep:*

5: /cgn2_6/pdataa/1/paa/us10_new_comb.pep:*

6: /cgn2_6/pdataa/1/paa/us60_NEW_COMBO.pep:*

7: /cgn2_6/pdataa/1/paa/us60_NEW_COMBO.pep:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1321	98.4	370	7 US-60-443-566-3011	Sequence 3011, AP
2	1124	83.7	1431	1 PCT-US03-02484-38	Sequence 38, Appl
3	1124	83.7	1431	5 US-09-944-002-377	Sequence 377, App
4	1124	83.7	1431	6 US-10-341-119-220	Sequence 220, App
5	1124	83.7	1436	7 US-60-443-566-4055	Sequence 4055, App
6	1121	83.5	282	5 US-09-724-676-69504	Sequence 69504, A
7	1121	83.5	282	5 US-09-724-676-69504	Sequence 69504, A
8	1121	83.5	454	1 PCT-US02-31357-119	Sequence 119, App
9	1121	83.5	454	6 US-10-263-445-119	Sequence 119, App
10	1121	83.5	454	7 US-60-443-566-2831	Sequence 2831, App
11	1121	83.5	595	5 US-09-724-676-69505	Sequence 65505, A
12	1121	83.5	595	5 US-09-724-676-69506	Sequence 65506, A
13	1087	80.9	1412	5 US-09-943-002-486	Sequence 486, App
14	660.5	49.2	2783	6 US-10-369-493-6344	Sequence 6344, App
15	663.8	47.5	414	7 US-60-443-566-2540	Sequence 240, App
16	636.5	47.4	508	6 US-10-271-978-18	Sequence 18, Appl
17	635.5	47.4	508	6 US-10-271-978-19	Sequence 19, Appl
18	625	46.5	372	7 US-60-443-566-2980	Sequence 2980, App
19	540.2	59.6	6 US-10-311-034-6	Sequence 6, Appl	
20	514	38.3	355	6 US-10-259-106-11	Sequence 11, Appl
21	514	38.3	355	6 US-10-355-975-10	Sequence 10, Appl
22	514	38.3	357	7 US-60-439-108-2	Sequence 2, Appl
23	514	38.3	357	7 PCT-US02-40194-15	Sequence 38, Appl
24	509	37.9	473	1 PCT-US02-40194-15	Sequence 15, Appl
25	37.2	37.9	473	1 US-10-320-315-15	Sequence 15, Appl
26	6	37.9	473	1 US-10-274-978-15	Sequence 15, Appl

RESULT 1	US-60-443-566-3011	98.4%; Score 1321; DB 7; Length 370;
Matches 260; Conservative	98.9%; Pred NO. 3, 6-120; 1; Mismatches 2; Indels 0; Gaps 0;	
QY	1 YDGEELGSGQFAIVKKCRE.....LVKHTRKRLTIQEALRHPWI 285	
Db	23 YDGEELGSGQFAIVKKCRE.....LVKHTRKRLTIQEALRHPWI 285	
QY	61 HNVITLHVYENRTDVWILEVSGGEFLDAQKESLSEERATSKFQLDGVNLT 120	
Db	143 KKHFDLKPKENIMLDKNIPIPKLFGLAHEIEGVFKNIFGPEFAI	
QY	181 PLGLEADWMSIGVITYILSAGSPFLGQKETLANTSVSYDFEEFSHSELAKFI 240	
Db	203 PLGLEADWMSIGVITYILSAGSPFLGQKETLANTSVSYDFEEFSHSELAKFI 262	

RESULT 2

PCT-US03-02484-38

; Sequence 38, Application PC/TUS0302484

; GENERAL INFORMATION:

; APPLICANT: Millennium Pharmaceuticals Inc.

APPLICANT: Carroll, Joseph M.
 APPLICANT: Healy, Aileen
 APPLICANT: Welch, Nadine S.
 APPLICANT: Kelly, Louise M.
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
 TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 146, 199, 12393, 13906,
 TITLE OF INVENTION: 1513, 17822, 302, 5677, 194, 14333, 28059, 7366, 12212,
 TITLE OF INVENTION: 191, 261, 12416, 270, 1410, 137, 1871, 13051, 1847, 1849,
 TITLE OF INVENTION: 15402, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES
 FILE REFERENCE: MPI0-010-019
 CURRENT APPLICATION NUMBER: PCT/US03/02484
 CURRENT FILING DATE: 2003-01-28
 PRIOR APPLICATION NUMBER: US 60/354, 333
 PRIOR FILING DATE: 2002-02-04
 PRIOR APPLICATION NUMBER: US 60/360, 258
 PRIOR FILING DATE: 2002-02-28
 PRIOR APPLICATION NUMBER: US 60/364, 476
 PRIOR FILING DATE: 2002-03-15
 PRIOR APPLICATION NUMBER: US 60/375, 626
 PRIOR FILING DATE: 2002-04-26
 PRIOR APPLICATION NUMBER: US 60/386, 494
 PRIOR FILING DATE: 2002-06-06
 PRIOR APPLICATION NUMBER: US 60/390, 965
 PRIOR FILING DATE: 2002-06-24
 PRIOR APPLICATION NUMBER: US 60/392, 480
 PRIOR FILING DATE: 2002-06-28
 PRIOR APPLICATION NUMBER: US 60/394, 128
 PRIOR FILING DATE: 2002-07-03
 PRIOR APPLICATION NUMBER: US 60/399, 783
 PRIOR FILING DATE: 2002-07-31
 PRIOR APPLICATION NUMBER: US 60/403, 221
 PRIOR FILING DATE: 2002-08-13
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 62
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 38
 LENGTH: 1431
 TYPE: PRT
 ORGANISM: Homo sapiens
 PCT-US03/02484-38

Query Match 83.7%; Score 1124; DB 1; length 1431;
 Best Local Similarity 79.5%; Pred. No. 3.9e-100; Gaps 0;
 Matches 209; Conservative 41; Mismatches 13; Indels 0; Gaps 0;

Qy 1 YDIGEELGGQFAIVKKCREKSTGLEYAAKFKKRROSRSRGSRSRETEREVSIQLQVL 60
 Db 13 YDGEELGGQFAIVKKCREKSTGLEYAAKFKKRROSRSRGSRSRETEREVSIQLQVL 72
 Qy 61 HHNVITLHWYENTDVHILELYSGGEFLAQAKESSEETSFVKQIOLGVNYIHT 120
 Db 73 HPNVITLHWYENTDVHILELYSGGEFLAQAKESLEETAEFLQIOLGVYYLHS 132
 Qy 121 KKAIFDFLKPFENTMLDKNIPHIKLFGLAHIEIDGVFKNIGPPEFVAPRIVYE 180
 Db 133 LQIAHFDFLKPFENTMLDKNIPHIKLFGLAHIKDGFNEKNIFGTPPEFVAPRIVYE 192
 Qy 181 PLGLRADMWASGVVYLISLGASPLFGDQKETQELANITSVYDEEFSTSALAKFI 240
 Db 193 PLGLRADMWASGVVYLISLGASPLFGDQKETQELANVSAVNEYEEDEFSNTSALAKDFI 252
 Qy 241 RKLKVKETRRLTQEAFLRHPWI 263
 Db 253 RRLLVKDPKKRMTODSLQHFWI 275

RESULT 4
 US-10-348-119-220
 ; Sequence 220, Application US/10348119
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTIVE
 ; TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASE PATHWAYS
 ; TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
 ; FILE REFERENCE: DOI185 NP
 ; CURRENT APPLICATION NUMBER: US/10/348,119
 ; CURRENT FILING DATE: 2003-01-17
 ; PRIOR APPLICATION NUMBER: US 60/350, 061
 ; PRIOR FILING DATE: 2002-01-18
 ; NUMBER OF SEQ ID NOS: 795
 ; SOFTWARE: Patentin version 3.2
 ; SEQ ID NO: 220
 ; LENGTH: 1431
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-348-119-220

Query Match 83.7%; Score 1124; DB 6; length 1431;
 Best Local Similarity 79.5%; Pred. No. 3.9e-100; Gaps 0;
 Matches 209; Conservative 41; Mismatches 13; Indels 0; Gaps 0;

Qy 1 YDGEELGGQFAIVKKCREKSTGLEYAAKFKKRROSRSRGSRSRETEREVSIQLQVL 60
 Db 13 YDGEELGGQFAIVKKCREKSTGLEYAAKFKKRROSRSRGSRSRETEREVSIQLQVL 72
 Qy 61 HHNVITLHWYENTDVHILELYSGGEFLAQAKESSEETSFVKQIOLGVNYIHT 120
 Db 73 HPNVITLHWYENTDVHILELYSGGEFLAQAKESLEETAEFLQIOLGVYYLHS 132
 Qy 121 KKAIFDFLKPFENTMLDKNIPHIKLFGLAHIEIDGVFKNIGPPEFVAPRIVYE 180
 Db 133 LQIAHFDFLKPFENTMLDKNIPHIKLFGLAHIKDGFNEKNIFGTPPEFVAPRIVYE 192
 Qy 181 PLGLRADMWASGVVYLISLGASPLFGDQKETQELANITSVYDEEFSTSALAKFI 240
 Db 193 PLGLRADMWASGVVYLISLGASPLFGDQKETQELANVSAVNEYEEDEFSNTSALAKDFI 252
 Qy 241 RKLKVKETRRLTQEAFLRHPWI 263
 Db 253 RRLLVKDPKKRMTODSLQHFWI 275

RESULT 5 ; LOCATION: (276)..(276)
 Db 133 LQIAHFDLKPKENIMLDKRNVPKRKIDFGIAHKIDFGNEKNIGTPFPEVAPETVNYE 192 ; OTHER INFORMATION: xaa can be any naturally occurring amino acid
 Qy 181 PGLEADMSIGVITYILSGASPFGLDTKQELTANLAVSNTAVNFEDYFSNTSELAKDFI 240 US-09-724-676-69504
 Db 193 PGLEADMSIGVITYILSGASPFGLDTKQELTANLAVSNTAVNFEDYFSNTSELAKDFI 252
 Qy 241 RKLKVKEPRKRKTQEAIRHPWI 263
 Db 253 RRLVKDKPDKRMTQDSLQHPWI 275

RESULT 5 ; GENERAL INFORMATION:
 US-60-443-566-4055 Sequence 4055, Application US/60443566
 ; APPLICANT: CARGILL, Michele
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH FILE REFERENCE: C1001447 CURRENT APPLICATION NUMBER: US/60/443, 566 CURRENT FILING DATE: 2003-01-30 NUMBER OF SEQ ID NOS: 25102 SOFTWARE: FastSEQ For Windows Version 4.0 SEQ ID NO: 4055 LENGTH: 1436 TYPE: PRT ORGANISM: Homo sapiens US-60-443-566-4055

Query Match Score 83.7%; Best Local Similarity 79.5%; Pred. No. 3.9e-10; Matches 209; Conservative 41; Mismatches 13; Indels 0; Gaps 0;

Qy 1 YDGEELGGSGQFAIVKKREKSTGGLEYAAFKRKQSRSRGSRRGVSREIERVSYLQVL 60 Db 13 YDGEELGGSGQFAIVKKREKSTGGLEYAAFKRKQSRSRGSRRGVSREIERVSYLQVL 72

Qy 61 HNNVITLHDVNRTDVHILEVSGGELDFLAQKESLSEETSFQKILDGVNLYHT 120 Db 73 HNNVITLHDVNRTDVHILEVSGGELDFLAQKESLSEETSFQKILDGVNLYHT 132

Qy 121 KKAHFDLKPKENIMLDKRNVPKRKIDFGIAHKIDFGNEKNIGTPFPEVAPETVNYE 180 Db 133 KKAHFDLKPKENIMLDKRNVPKRKIDFGIAHKIDFGNEKNIGTPFPEVAPETVNYE 192

Qy 181 PGLEADMSIGVITYILSGASPFGLDTKQELTANLAVSNTAVNFEDYFSNTSELAKDFI 240 Db 193 PGLEADMSIGVITYILSGASPFGLDTKQELTANLAVSNTAVNFEDYFSNTSELAKDFI 252

Qy 241 RKLKVKEPRKRKTQEAIRHPWI 263 Db 253 RRLVKDKPDKRMTQDSLQHPWI 275

RESULT 7 ; GENERAL INFORMATION:
 US-09-724-676A-69504 Sequence 69504, Application US/09724676A
 ; APPLICANT: Compugen LTD
 ; TITLE OF INVENTION: Variants of alternative splicing FILE REFERENCE: 129181.4 CURRENT APPLICATION NUMBER: US/09/724, 676A CURRENT FILING DATE: 2000-11-28 NUMBER OF SEQ ID NOS: 97222 SOFTWARE: Patentin version 3.2 SEQ ID NO: 69504 LENGTH: 282 TYPE: PRT ORGANISM: Homo sapiens FEATURE: NAMEKEY: misc_feature LOCATION: (275)..(276) OTHER INFORMATION: Xaa can be any naturally occurring amino acid US-09-724-676A-69504

Query Match Score 83.5%; Best Local Similarity 79.8%; Pred. No. 6.5e-101; Matches 210; Conservative 36; Mismatches 17; Indels 0; Gaps 0;

Qy 1 YDGEELGGSGQFAIVKKREKSTGGLEYAAFKRKQSRSRGSRRGVSREIERVSYLQVL 60 Db 13 YDGEELGGSGQFAIVKKREKSTGGLEYAAFKRKQSRSRGSRRGVSREIERVSYLQVL 72

Qy 61 HNNVITLHDVNRTDVHILEVSGGELDFLAQKESLSEETSFQKILDGVNLYHT 120 Db 73 HNNVITLHDVNRTDVHILEVSGGELDFLAQKESLSEETSFQKILDGVNLYHT 132

Qy 121 KKAHFDLKPKENIMLDKRNVPKRKIDFGIAHKIDFGNEKNIGTPFPEVAPETVNYE 180 Db 133 KKAHFDLKPKENIMLDKRNVPKRKIDFGIAHKIDFGNEKNIGTPFPEVAPETVNYE 192

Qy 181 PGLEADMSIGVITYILSGASPFGLDTKQELTANLAVSNTAVNFEDYFSNTSELAKDFI 240 Db 193 PGLEADMSIGVITYILSGASPFGLDTKQELTANLAVSNTAVNFEDYFSNTSELAKDFI 252

Qy 241 RKLKVKEPRKRKTQEAIRHPWI 263 Db 253 RRLVKDKPDKRMTQDSLQHPWI 275

RESULT 6 ; GENERAL INFORMATION:
 US-09-724-676-69504 Sequence 69504, Application US/09724676 ; APPLICANT: Compugen LTD
 ; TITLE OF INVENTION: Variants of alternative splicing FILE REFERENCE: 129181.4 Compugen CURRENT APPLICATION NUMBER: US/09/724, 676 CURRENT FILING DATE: 2000-11-28 NUMBER OF SEQ ID NOS: 97222 SOFTWARE: Patentin version 3.2 SEQ ID NO: 69504 LENGTH: 282 TYPE: PRT ORGANISM: Homo sapiens FEATURE: NAMEKEY: misc_feature LOCATION: (275)..(276) OTHER INFORMATION: Xaa can be any naturally occurring amino acid US-09-724-676-69504

Query Match Score 83.5%; Best Local Similarity 79.8%; Pred. No. 6.5e-101; Matches 210; Conservative 36; Mismatches 17; Indels 0; Gaps 0;

Qy 1 YDGEELGGSGQFAIVKKREKSTGGLEYAAFKRKQSRSRGSRRGVSREIERVSYLQVL 60 Db 13 YDGEELGGSGQFAIVKKREKSTGGLEYAAFKRKQSRSRGSRRGVSREIERVSYLQVL 72

Qy 61 HNNVITLHDVNRTDVHILEVSGGELDFLAQKESLSEETSFQKILDGVNLYHT 120 Db 73 HNNVITLHDVNRTDVHILEVSGGELDFLAQKESLSEETSFQKILDGVNLYHT 132

Qy 121 KKAHFDLKPKENIMLDKRNVPKRKIDFGIAHKIDFGNEKNIGTPFPEVAPETVNYE 180 Db 133 KKAHFDLKPKENIMLDKRNVPKRKIDFGIAHKIDFGNEKNIGTPFPEVAPETVNYE 192

Qy 181 PGLEADMSIGVITYILSGASPFGLDTKQELTANLAVSNTAVNFEDYFSNTSELAKDFI 240 Db 193 PGLEADMSIGVITYILSGASPFGLDTKQELTANLAVSNTAVNFEDYFSNTSELAKDFI 252

Qy 241 RKLKVKEPRKRKTQEAIRHPWI 263 Db 253 RRLVKDKPDKRMTQDSLQHPWI 275

NAME/KEY: misc_feature

RESULT 8
; Sequence 119, Application PC/TUS0231357
; GENERAL INFORMATION:
; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS C
; FILE REFERENCE: 21402-462D-061
; CURRENT APPLICATION NUMBER: PCT/US02/31357
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/327,454
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,849
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/329,414
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/330,142
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 60/331,058
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/343,629
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/349,575
; PRIOR FILING DATE: 2001-10-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO: 119
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-US02-31357-119

Query Match 83.5%; Score 1121; DB 1; Length 454;
Best Local Similarity 79.8%; Pred. No. 1. 3e-100; Mismatches 210; Conservative 36; Indels 0; Gaps 0;

Qy 1 YDIGEELGGSGOFAIVRKCREKSTGLEYAAKKIKRKRSSRASRGVSREITEREVSIHQVL 60
Db 13 YEMGEELGGSGOFAIVRKCRQKGTKGEYAAKKIKRKLSSRRGSVSREIEREVNIIREIR 72
Db 13 YEMGEELGGSGOFAIVRKCRQKGTKGEYAAKKIKRKLSSRRGSVSREIEREVNIIREIR 72

Qy 61 HHNWITLHDVYENRTDVHILELVSGELFLAKESLSSEATSFIKIQILDGVNLHT 120
Db 73 HPNIIITLHDIFENKTDVVLILEBLVSGGELDFLAEKESLTDEATOFLQIQLDGVHLHS 132

Qy 121 KTAHFDLKPENIMLDKNIPHIKILDFGLAHETEDGVFKNFGTPPEVAPENVYE 180
Db 133 KTAHFDLKPENIMLDKNIPHIKILDFGLAHETEDGVFKNFGTPPEVAPENVYE 192

Qy 181 PIGLEADMWSIGVITYILLSGASPFLEGTQETLNTISVSYDFDEFFSITSELAKDFI 240
Db 193 PIGLEADMWSIGVITYILLSGASPFLEGTQETLNTISVSYDFDEFFSITSELAKDFI 252

Qy 241 RKLKVKETRKRKLTIQEALRHPI 263
Db 253 RRLUVKDPKRRMTIAQSLEHNSI 275

RESULT 9
US-10-262-445-119
; Sequence 119, Application US/10262445
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John
; APPLICANT: Burgess, Catherine
; APPLICANT: Catterton, Elina

APPLICANT: Chant, John
APPLICANT: Chaudhuri, Amitabha
APPLICANT: Edinger, Shlonit
APPLICANT: Gerlach, Valerie
APPLICANT: Giot, Loic
APPLICANT: Gorman, Linda
APPLICANT: Guo, Xiaojia
APPLICANT: Kekua, Ramesh
APPLICANT: Mezes, Peter
APPLICANT: Millet, Isabelle
APPLICANT: Spytek, Kimberly
APPLICANT: Taupier Jr., Raymond J.
APPLICANT: Zerhusen, Bryan
APPLICANT: Zhong, Haifeng
APPLICANT: Zhou, Mei
TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHOD
FILE REFERENCE: THE SAME
CURRENT APPLICATION NUMBER: US/10-262,445
CURRENT FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/328,056
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/328,849
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/329,414
PRIOR FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 60/330,142
PRIOR FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: 60/331,058
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: 60/343,629
PRIOR FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 60/349,575
PRIOR FILING DATE: 2001-10-29
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 133
SOFTWARE: CuraseqList version 0.1
SEQ ID NO: 119
LENGTH: 454
TYPE: PRT
ORGANISM: Homo sapiens
US-10-262-445-119

Query Match 83.5%; Score 1121; DB 6; Length 454;
Best Local Similarity 79.8%; Pred. No. 1. 3e-100; Mismatches 210; Conservative 36; Indels 0; Gaps 0;

Qy 1 YDIGEELGGSGOFAIVRKCREKSTGLEYAAKKIKRKRSSRASRGVSREITEREVSIHQVL 60
Db 13 YEMGEELGGSGOFAIVRKCRQKGTKGEYAAKKIKRKLSSRRGSVSREIEREVNIIREIR 72
Db 13 YEMGEELGGSGOFAIVRKCRQKGTKGEYAAKKIKRKLSSRRGSVSREIEREVNIIREIR 72

Qy 61 HHNWITLHDVYENRTDVHILELVSGELFLAKESLSSEATSFIKIQILDGVNLHT 120
Db 73 HPNIIITLHDIFENKTDVVLILEBLVSGGELDFLAEKESLTDEATOFLQIQLDGVHLHS 132

Qy 121 KTAHFDLKPENIMLDKNIPHIKILDFGLAHETEDGVFKNFGTPPEVAPENVYE 180
Db 133 KTAHFDLKPENIMLDKNIPHIKILDFGLAHETEDGVFKNFGTPPEVAPENVYE 192

Qy 181 PIGLEADMWSIGVITYILLSGASPFLEGTQETLNTISVSYDFDEFFSITSELAKDFI 240
Db 193 PIGLEADMWSIGVITYILLSGASPFLEGTQETLNTISVSYDFDEFFSITSELAKDFI 252

Qy 241 RKLKVKETRKRKLTIQEALRHPI 263

Db 253 RRLUVKDPKRRTIAQSLEHSMWI 275

RESULT 10

; Sequence 2831, Application US/60443566

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL00147

CURRENT APPLICATION NUMBER: US/60/443, 566

CURRENT FILING DATE: 2003-01-30

NUMBER OF SEQ ID NOS: 25102

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 2831

LENGTH: 454

TYPE: PRT

ORGANISM: Homo sapiens

US-60-443-566-2831

Query Match 83.5%; Score 1121; DB 7; Length 454;

Best Local Similarity 79.8%; Pred. No. 1. 3e-100; Matches 210; Conservative 36; Mismatches 17; Indels 0; Gaps 0;

Qy 1 YDGEELGSQFAIVKRCRKGTGKEYAKFKKRLLSSRRGVREELIREIR 72

Db 13 YEMGEELGSQFAIVKRCRKGTGKEYAKFKKRLLSSRRGVREELIREIR 72

Qy 61 HNVVITLHDYENRTDVHILEVLVGELDFLAOKRESSEEAATSPFKQILDGVNLHT 120

Db 73 HPNITLHDIFENKTDVILEVLVGELDFLAKESTEDATEQFLQILDGVYHLS 132

Qy 121 KKAHDPLKPEIMLDDKNPKPHKLIDGLAHEDEGYEFKNGTPEVAPEVNYE 180

Db 133 KRAHFDLKPEIMLDDKNPKHLPKIDFGIAHKTEAGNEKFKNIFGTPPEVAPEVNYE 192

Qy 181 PGLEADMWSIGVITYILSGASPFGLDTKOETLTANITSYSDFBEFFSHTEAKDFI 240

Db 193 PGLEADMWSIGVITYILSGASPFGLDTKOETLTANITSYSDFBEFFSHTEAKDFI 252

Qy 241 RKLVKETRKRLTIQEALRHPWI 263

Db 253 RRLUVKDPKRRTIAQSLEHSMWI 275

RESULT 11

US-09-724-676-69506

; Sequence 69506, Application US/09724676

; GENERAL INFORMATION:

; APPLICANT: Compugen LTD

; TITLE OF INVENTION: Variants of alternative splicing

FILE REFERENCE: 129181.4 Compugen LTD

CURRENT APPLICATION NUMBER: US/09/724, 676A

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patentin version 3.2

SEQ ID NO: 69506

LENGTH: 595

TYPE: PRT

ORGANISM: Homo sapiens

US-09-724-676A-69506

Query Match 83.5%; Score 1121; DB 5; Length 595;

Best Local Similarity 79.8%; Pred. No. 2e-100; Matches 210; Conservative 36; Mismatches 17; Indels 0; Gaps 0;

Qy 1 YDGEELGSQFAIVKRCRKGTGKEYAKFKKRLLSSRRGVREELIREIR 72

Db 13 YEMGEELGSQFAIVKRCRKGTGKEYAKFKKRLLSSRRGVREELIREIR 72

Qy 61 HNVVITLHDYENRTDVHILEVLVGELDFLAOKRESSEEAATSPFKQILDGVNLHT 120

Db 73 HPNITLHDIFENKTDVILEVLVGELDFLAKESTEDATEQFLQILDGVYHLS 132

Qy 121 KKAHDPLKPEIMLDDKNPKPHKLIDGLAHEDEGYEFKNGTPEVAPEVNYE 180

Db 133 KRAHFDLKPEIMLDDKNPKHLPKIDFGIAHKTEAGNEKFKNIFGTPPEVAPEVNYE 192

Qy 181 PGLEADMWSIGVITYILSGASPFGLDTKOETLTANITSYSDFBEFFSHTEAKDFI 240

Db 193 PGLEADMWSIGVITYILSGASPFGLDTKOETLTANITSYSDFBEFFSHTEAKDFI 252

Qy 241 RKLVKETRKRLTIQEALRHPWI 263

Db 253 RRLUVKDPKRRTIAQSLEHSMWI 275

RESULT 12

US-09-724-676A-69506

; Sequence 69506, Application US/09724676A

; GENERAL INFORMATION:

; APPLICANT: Compugen LTD

; TITLE OF INVENTION: Variants of alternative splicing

FILE REFERENCE: 129181.4 Compugen LTD

CURRENT APPLICATION NUMBER: US/09/724, 676A

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patentin version 3.2

SEQ ID NO: 69506

LENGTH: 595

TYPE: PRT

ORGANISM: Homo sapiens

US-09-724-676A-69506

Query Match 83.5%; Score 1121; DB 5; Length 595;

Best Local Similarity 79.8%; Pred. No. 2e-100; Matches 210; Conservative 36; Mismatches 17; Indels 0; Gaps 0;

Qy 1 YDGEELGSQFAIVKRCRKGTGKEYAKFKKRLLSSRRGVREELIREIR 72

Db 13 YEMGEELGSQFAIVKRCRKGTGKEYAKFKKRLLSSRRGVREELIREIR 72

Qy 61 HNVVITLHDYENRTDVHILEVLVGELDFLAOKRESSEEAATSPFKQILDGVNLHT 120

Db 73 HPNITLHDIFENKTDVILEVLVGELDFLAKESTEDATEQFLQILDGVYHLS 132

Qy 121 KKAHDPLKPEIMLDDKNPKPHKLIDGLAHEDEGYEFKNGTPEVAPEVNYE 180

Db 133 KRAHFDLKPEIMLDDKNPKHLPKIDFGIAHKTEAGNEKFKNIFGTPPEVAPEVNYE 192

Qy 181 PGLEADMWSIGVITYILSGASPFGLDTKOETLTANITSYSDFBEFFSHTEAKDFI 240

Db 193 PGLEADMWSIGVITYILSGASPFGLDTKOETLTANITSYSDFBEFFSHTEAKDFI 252

Qy 241 RKLVKETRKRLTIQEALRHPWI 263

Db 253 RRLUVKDPKRRTIAQSLEHSMWI 275

RESULT 13

US-09-949-002-486

; Sequence 486, Application US/09949002

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH INFLAMMATION, AND USES THEREOF

FILE REFERENCE: CL000790

CURRENT APPLICATION NUMBER: US/09/949, 002

CURRENT FILING DATE: 2000-01-28

PRIOR APPLICATION NUMBER: 60/231, 401

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 10823

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO: 486 LENGTH: 1412 TYPE: PRT ORGANISM: Human ; US-09-949-002-486

Query Match 80.9%; Score 1087; DB 5; Length 1412; Best Local Similarity 79.0%; Pred. No. 1..5e-96; Matches 203; Conservative 41; Mismatches 13; Indels 0; Gaps 0;

Qy 7 LGSQFAIVKKCREKSTGLEYAAFKIKKRQSARSGRSVRETEREVSIILROVLHNVIT 66 Db 1 LFSQGQFAIVKKCREKSTGLEYAAFKIKKRQSARSGRSVRETEREVSIILROVLHNVIT 66 ; APPLICANT: BEGOVICH, Ann ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH FILE REFERENCE: C100147 CURRENT APPLICATION NUMBER: US/60/443, 566 ; CURRENT FILING DATE: 2003-01-30 ; NUMBER OF SEQ ID NOS: 25102 ; SOFTWARE: FASTSEQ for Windows Version 4.0 ; SEQ ID NO: 2540 ; LENGTH: 414 ; TYPE: PRT ; ORGANISM: Homo sapiens US-60-443-566-2540

RESULT 14

US-10-369-493-6344

Sequence 6344, Application US/10369493

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369, 493

PRIOR APPLICATION NUMBER: US 60/360, 039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 4734

SEQ ID NO 6344

LENGTH: 2783

TYPE: PRT

ORGANISM: Caenorhabditis elegans ; US-10-369-493-6344

Query Match 49.2%; Score 660.5; DB 6; Length 2783; Best Local Similarity 47.3%; Pred. No. 1.2e-54; Matches 125; Conservative 61; Mismatches 9; Indels 3; Gaps 3;

Qy 1 YDGEELGGQFAIVKKCREKSTGLEYAAFKIKKRQSARSGRSVRETEREVSIILROVLHNVIT 60 Db 195 YDGEELGGQFAIVKKCREKSTGLEYAAFKIKKRQSARSGRSVRETEREVSIILROVLHNVIT 60 ; APPLICANT: Cargill, Michele ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH FILE REFERENCE: C100147 CURRENT APPLICATION NUMBER: US/60/443, 566 ; CURRENT FILING DATE: 2003-01-30 ; NUMBER OF SEQ ID NOS: 25102 ; SOFTWARE: FASTSEQ for Windows Version 4.0 ; SEQ ID NO: 2540 ; LENGTH: 414 ; TYPE: PRT ; ORGANISM: Homo sapiens US-60-443-566-2540

Query Match 47.5%; Score 638; DB 7; Length 414; Best Local Similarity 46.0%; Pred. No. 1e-53; Matches 122; Conservative 65; Mismatches 65; Indels 12; Gaps 6;

Qy 4 GEELGGQFAIVKKCREKSTGLEYAAFKIKKRQSARSGRSVRETEREVSIILROVLHNVIT 62 Db 64 GRELGRCGKFAVVKRCKIKRDSKEFARKEMRKR---RKGDCCRMEIHEAVL-EIAQD 117 ; APPLICANT: Cargill, Michele ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369, 493

PRIOR APPLICATION NUMBER: US 60/360, 039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 4734

SEQ ID NO 6344

LENGTH: 2783

TYPE: PRT

ORGANISM: Caenorhabditis elegans ; US-10-369-493-6344

Search completed: March 26, 2003, 19:17:07 Job time : 24.6854 secs